

cat cag tgg gaa aat aca cct tta aaa gca gaa aga cat aga act gaa His Gln Trp Glu Asn Thr Pro Leu Lys Ala Glu Arg His Arg Thr Glu	455	460	465	470	1624
gat aag aga aaa aga gaa caa gaa agc aaa gaa gaa aat agg cat att Asp Lys Arg Lys Arg Glu Gln Glu Ser Lys Glu Glu Asn Arg His Ile	471	476	481	486	1672
aga aat gaa aaa aga gta cct aca gaa cat ttg cag aag act aat aag Arg Asn Glu Lys Arg Val Pro Thr Glu His Leu Gln Lys Thr Asn Lys	487	492	497	502	1720
gaa act aag aaa acc act act gat tta aag aaa cag aat gaa cca aag Glu Thr Lys Lys Thr Thr Asp Leu Lys Lys Gln Asn Glu Pro Lys	503	508	513	518	1768
act gat aag gga gaa gtc ctt gat aat ggt gtt tct gaa gga gca gat Thr Asp Lys Gly Glu Val Leu Asp Asn Gly Val Ser Glu Gly Ala Asp	519	524	529	534	1816
aat aaa gag ctt gca atg aaa gct gag agt ggt cca aat gaa aca aaa Asn Lys Glu Leu Ala Met Lys Ala Glu Ser Gly Pro Asn Glu Thr Lys	535	540	545	550	1864
aac aag gac cta aaa ttg agt ttt atg aaa aaa ttg aac tta act ctt Asn Lys Asp Leu Lys Leu Ser Phe Met Lys Lys Leu Asn Leu Thr Leu	551	556	561	566	1912
tct cct gct aaa aag caa cct gtt tcc cag gat aat cag cat aaa ata Ser Pro Ala Lys Lys Gin Pro Val Ser Gln Asp Asn Gln His Lys Ile	567	572	577	582	1960
act gat att ccc aag tcc agt ggt gta tgt gat tca gag tct tca atg Thr Asp Ile Pro Lys Ser Ser Gly Val Cys Asp Ser Glu Ser Ser Met	583	588	593	598	2008
caa gtt aaa aca gtg gca tat gtt ccc tcc ata agt gaa cat atc ttg Gln Val Lys Thr Val Ala Tyr Val Pro Ser Ile Ser Glu His Ile Leu	599	604	609	614	2056
ggg gaa gca gct gtc agt gaa cat acc atg ggg gaa acc aag tca acg Gly Glu Ala Ala Val Ser Glu His Thr Met Gly Glu Thr Lys Ser Thr	615	620	625	630	2104
tta ttg gaa cca aag gtt gct ctt cta gca gtg act gaa ccc agg atc Leu Leu Glu Pro Lys Val Ala Leu Leu Ala Val Thr Glu Pro Arg Ile	631	636	641	646	2152
ggt atc tca gaa acc aac aag gaa gac gaa aat agt ttg tta gtt agg Gly Ile Ser Glu Thr Asn Lys Glu Asp Glu Asn Ser Leu Leu Val Arg	647	652	657	662	2200
tct gtt gac aat act atg cat tgt gaa gag ccc att tgt ggt aca gag Ser Val Asp Asn Thr Met His Cys Glu Glu Pro Ile Cys Gly Thr Glu	663	668	673	678	2248
act tcc ttc cca tct cct atg gaa ata caa cag aca gaa tcc ttg ttt					2296

Thr Ser Phe Pro Ser Pro Met Glu Ile Gln Gln Thr Glu Ser Leu Phe			
679	684	689	694
cca tca aca gga atg aaa caa acc att aat aat gga agg gca gca gct			2344
Pro Ser Thr Gly Met Lys Gln Thr Ile Asn Asn Gly Arg Ala Ala Ala			
695	700	705	710
cct gtg gta atg gat gta tta caa aca gat gtg tct caa aac ttt ggc			2392
Pro Val Val Met Asp Val Leu Gln Thr Asp Val Ser Gln Asn Phe Gly			
711	716	721	726
ttg gaa ttg gat acc aaa aga aat gat aat tca gat tat tgt ggt att			2440
Leu Glu Leu Asp Thr Lys Arg Asn Asp Asn Ser Asp Tyr Cys Gly Ile			
727	732	737	742
tct gaa ggt atg gag atg aag gtg gca ctt tca aca aca gtg agt gaa			2488
Ser Glu Gly Met Glu Met Lys Val Ala Leu Ser Thr Thr Val Ser Glu			
743	748	753	758
acc act gaa agc att ttg cag cct tca att gag gaa gct gat att ttg			2536
Thr Thr Glu Ser Ile Leu Gln Pro Ser Ile Glu Glu Ala Asp Ile Leu			
759	764	769	774
cca ata atg ctt tca gaa gat aat aac cca aaa ttt gag cct tct gtt			2584
Pro Ile Met Leu Ser Glu Asp Asn Asn Pro Lys Phe Glu Pro Ser Val			
775	780	785	790
ata gtt aca cca ctg gtt gag agt aag tcg tgt cat ctg gag cct tgc			2632
Ile Val Thr Pro Leu Val Glu Ser Lys Ser Cys His Leu Glu Pro Cys			
791	796	801	806
tta cct aaa gag act cta gat tct tca ctt cag cag act gag tta atg			2680
Leu Pro Lys Glu Thr Leu Asp Ser Ser Leu Gln Gln Thr Glu Leu Met			
807	812	817	822
gac cac aga atg gca act ggt gaa aca aac tca gta tat cat gat gat			2728
Asp His Arg Met Ala Thr Gly Glu Thr Asn Ser Val Tyr His Asp Asp			
823	828	833	838
gat aac tcg gtt ttg agc att gac ctt aat cac ctg aga cct att cca			2776
Asp Asn Ser Val Leu Ser Ile Asp Leu Asn His Leu Arg Pro Ile Pro			
839	844	849	854
gaa gcc atc agt cct ctg aat agt cca gtg aga cct gta gca aaa gtt			2824
Glu Ala Ile Ser Pro Leu Asn Ser Pro Val Arg Pro Val Ala Lys Val			
855	860	865	870
ctt aga aat gaa agc cca cct caa gtt cca gtg tat aat aac agt cat			2872
Leu Arg Asn Glu Ser Pro Pro Gln Val Pro Val Tyr Asn Asn Ser His			
871	876	881	886
aaa gat gtg ttt tta cca aat tca gct cat tct acc tct aag agt cag			2920
Lys Asp Val Phe Leu Pro Asn Ser Ala His Ser Thr Ser Lys Ser Gln			
887	892	897	902
tct gat ctc aat aag gaa aat caa aag cca att tac aaa tct gac aaa			2968
Ser Asp Leu Asn Lys Glu Asn Gln Lys Pro Ile Tyr Lys Ser Asp Lys			

903	908	913	918	
tgt aca gaa gca gac aca tgt aag aat tca cca tta gat gaa tta gaa Cys Thr Glu Ala Asp Thr Cys Lys Asn Ser Pro Leu Asp Glu Leu Glu 919 924 929 934				3016
gaa gga gaa att aga agt gat agt gaa aca tct aaa cca caa gaa agt Glu Gly Glu Ile Arg Ser Asp Ser Glu Thr Ser Lys Pro Gln Glu Ser 935 940 945 950				3064
ttt gaa aaa aat tcc aaa cgt aga gtg tca gct gat gtg cggt aag tca Phe Glu Lys Asn Ser Lys Arg Arg Val Ser Ala Asp Val Arg Lys Ser 951 956 961 966				3112
aag act atc cca cga cgt ggg aaa agt act gtg tgt tta gat aaa gac Lys Thr Ile Pro Arg Arg Gly Lys Ser Thr Val Cys Leu Asp Lys Asp 967 972 977 982				3160
agt agg aaa aca cat gta aga atc cat cag acc aat aac aaa tgg aat Ser Arg Lys Thr His Val Arg Ile His Gln Thr Asn Asn Lys Trp Asn 983 988 993 998				3208
aaa aga cct gat aaa tct agt aga tct tca aaa aca gag aag aaa gat Lys Arg Pro Asp Lys Ser Ser Arg Ser Ser Lys Thr Glu Lys Lys Asp 999 1004 1009 1014				3256
aaa gtg atg agc act tcc agc ttg gaa aaa ata gtt cca att att gct Lys Val Met Ser Thr Ser Leu Glu Lys Ile Val Pro Ile Ile Ala 1015 1020 1025 1030				3304
gta ccc tct tct gaa caa gag atc atg cac atg tta cga atg ata aga Val Pro Ser Ser Glu Gln Glu Ile Met His Met Leu Arg Met Ile Arg 1031 1036 1041 1046				3352
aaa cat gta aga aaa aat tat atg aaa ttc aag gca aaa ttt tca tta Lys His Val Arg Lys Asn Tyr Met Lys Phe Lys Ala Lys Phe Ser Leu 1047 1052 1057 1062				3400
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tta att aaa cat ctc aac tta cac aaa atc tct aag tca gtg act acc Leu Ile Lys His Leu Asn Leu His Lys Ile Ser Lys Ser Val Thr Thr 1079 1084 1089 1094				3496
tta cag aag aat ctc tgt gat att ata gag tct aaa ctt aag caa gtt Leu Gln Lys Asn Leu Cys Asp Ile Ile Glu Ser Lys Leu Lys Gln Val 1095 1100 1105 1110				3544
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atg aaa aaa aat ttg tgg aag ttt gta gat gac caa ctt gat tat ttg Met Lys Lys Leu Trp Lys Phe Val Asp Asp Gln Leu Asp Tyr Leu 1127 1132 1137 1142				3640

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1223 1228 1233 1238	
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1239 1244 1249 1254	
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1255 1260 1265 1270	
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1287 1292 1297 1302	
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1303 1308 1313 1318	
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1319 1324 1329 1334	
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1351 1356 1361 1366	

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tca tct gaa aaa ggt cca tct ctg tct tca ggg ctt tca ttg ccg gtt Ser Ser Glu Lys Gly Pro Ser Leu Ser Ser Gly Leu Ser Leu Pro Val	1383	1388	1393	1398	4408
cat cct gat gtg ttg gat gaa agt tgt atg ttt gaa gtg tct act aac His Pro Asp Val Leu Asp Glu Ser Cys Met Phe Glu Val Ser Thr Asn	1399	1404	1409	1414	4456
cta cct tta agt aaa gat aat gtg tgt agt gta gaa aag agc aag ccc Leu Pro Leu Ser Lys Asp Asn Val Cys Ser Val Glu Lys Ser Lys Pro	1415	1420	1425	1430	4504
tgc gtt tct tcc ata ctt ctt gaa gat cta gca gtc tct tta aca gta Cys Val Ser Ser Ile Leu Leu Glu Asp Leu Ala Val Ser Leu Thr Val	1431	1436	1441	1446	4552
cca tcg cct ctg aag tca gat ggt cat ctc agt ttt tta aag cct gat Pro Ser Pro Leu Lys Ser Asp Gly His Leu Ser Phe Leu Lys Pro Asp	1447	1452	1457	1462	4600
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gaa gat gcc tta ctt gag gaa gag gat gca tct gag caa gat att cat Glu Asp Ala Leu Leu Glu Glu Asp Ala Ser Glu Gln Asp Ile His	1479	1484	1489	1494	4696
tta gct ctg gag tct gat aat tca agc agt aaa tca agt tgt tct tct Leu Ala Leu Glu Ser Asp Asn Ser Ser Lys Ser Ser Cys Ser Ser	1495	1500	1505	1510	4744
tcc tgg aca agc cga tct gtt gct cca ggc ttt cag tac cac cct aat Ser Trp Thr Ser Arg Ser Val Ala Pro Gly Phe Gln Tyr His Pro Asn	1511	1516	1521	1526	4792
cta cct atg cat gcc gtc ata atg gaa aag tcc aat gat cat ttc att Leu Pro Met His Ala Val Ile Met Glu Lys Ser Asn Asp His Phe Ile	1527	1532	1537	1542	4840
gtg aaa ata cga cgt gca aca cca tct acc tct tct ggc ctt aaa cag Val Lys Ile Arg Arg Ala Thr Pro Ser Thr Ser Ser Gly Leu Lys Gln	1543	1548	1553	1558	4888
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gaa gct gat gaa gga cca gag aaa gaa tat att tca tgt cag aac aca Glu Ala Asp Glu Gly Pro/Glu Lys Glu Tyr Ile Ser Cys Gln Asn Thr	1575	1580	1585	1590	4984
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Val Phe Lys Ser Val Glu Glu Leu Glu Asn Ser Asn Lys Asn Val Asp				
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1607	1612	1617	1622	
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1623	1628	1633	1638	
cat agt gat gaa gtg gct gat gaa tgt ttc aaa ttg cat caa gta tgg	His Ser Asp Glu Val Ala Asp Glu Cys Phe Lys Leu His Gln Val Trp			5176
1639	1644	1649	1654	
gaa aca aaa gtg cct gaa agc att gaa gaa ttg cct tca atg gaa gaa	Glu Thr Lys Val Pro Glu Ser Ile Glu Glu Leu Pro Ser Met Glu Glu			5224
1655	1660	1665	1670	
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1671	1676	1681	1686	
acg aaa gat cca gtc act gaa acc aaa aac ttg ggg gaa ttc ata gaa	Thr Lys Asp Pro Val Thr Glu Thr Lys Asn Leu Gly Glu Phe Ile Glu			5320
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gta aca gtt tta cat att gat cag ttg gga tgt tct gga ggc aat tta	Val Thr Val Leu His Ile Asp Gln Leu Gly Cys Ser Gly Gly Asn Leu			5368
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1719	1724	1729	1734	
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1751	1756	1761	1766	
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1815	1820	1825	1830	
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1847	1852	1857	1862	
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1863	1868	1873	1878	
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1879	1884	1889	1894	
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1911	1916	1921	1926	
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1943	1948	1953	1958	
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1959	1964	1969	1974	
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1975	1980			
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Met Ala Gly Asp Gly Arg Arg Ala Glu		
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Ala Val Arg Glu Gly Trp Gly Val Tyr Val Thr Pro	Arg Ala Pro Ile	
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Arg Glu Gly Arg Gly Arg Leu Ala Pro Gln Asn	Gly Gly Ser Ser Asp	
26 31 36 41		
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Ala Pro Ala Tyr Arg Thr Pro Pro Ser Arg Gln	Gly Arg Arg Glu Val	
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Arg Phe Ser Asp Glu Pro Pro Glu Val Tyr Gly	Asp Phe Glu Pro Leu	
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Val Ala Lys Glu Arg Ser Pro Val Gly Lys Arg	Thr Arg Leu Glu Glu	
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Phe Arg Ser Asp Ser Ala Lys Glu Glu Val Arg	Glu Ser Ala Tyr Tyr	
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298 303 308 313	
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Ile Gly Asn Ala Gly Glu Lys Ser Leu Ser Glu Asp Ala Lys Lys Lys	
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Lys Lys Ser Asn Arg Lys Glu Asp Asp Val Met Ala Ser Gly Thr Val	
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aaa cga cac cta aaa aca tct gga gaa tgt gaa cga aaa act aag aaa	846
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ctc atg gca gaa gtg gaa aat ctt cga aag cgt gtg ctt gaa atg gaa			1806
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424	429	434	439
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Glu Ala Phe Ser Lys Ser Glu Cys Thr Gln Leu His Leu Asn			
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ctg gag aaa gaa aag aac tta acc aaa gac ctg cta aat gaa ttg gag			2046
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Phe Thr Val Met Leu Val Asp Glu Arg Lys Asn Met Met Glu Lys Ile			
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Lys Gln Glu Glu Arg Lys Val Asp Gly Leu Asn Lys Asn Phe Lys Val			
520	525	530	535
gaa caa gga aaa gtt atg gat gta act gaa aaa cta att gaa agt			2286

Glu Gln Gly Lys Val Met Asp Val Thr Glu Lys Leu Ile Glu Glu Ser			
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Lys Lys Leu Leu Lys Leu Lys Ser Glu Met Glu Glu Lys Val Tyr Asn			
552	557	562	567
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Leu Thr Arg Glu Arg Asp Glu Leu Ile Gly Lys Leu Lys Ser Glu Glu			
568	573	578	583
gaa aaa tcc tct gaa tta agc tgc agt gtt gac tta cta aag aag aga			2430
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Arg Lys Gly Ser Glu Leu Thr Cys Pro Glu Asp Asn Lys Ile Lys Glu			
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776	781	786	791	
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Asn Tyr Ala Ala Ile Arg Ala Glu Tyr Ala Asp Arg His Ala Glu Leu		
528 533 538 543		
tct gga agt cca ctg aaa agc aaa agc act agg aag cct ttg gca tgt		1920

Ser	Gly	Ser	Pro	Leu	Lys	Ser	Lys	Ser	Thr	Arg	Lys	Pro	Leu	Ala	Cys	
544				549					554				559			
atc att ggg tat tta gag atc cat cct gca aag aaa cct aat gta att																1968
Ile	Ile	Gly	Tyr	Leu	Glu	Ile	His	Pro	Ala	Lys	Lys	Pro	Asn	Val	Ile	
560				565					570				575			
cga	tct	aca	cca	agc	ctg	caa	acc	cca	act	acc	aag	cgg	atg	cta	aca	
Arg	Ser	Thr	Pro	Ser	Leu	Gln	Thr	Pro	Thr	Thr	Lys	Arg	Met	Leu	Thr	
576				581					586				591			
act	cca	aat	cac	aca	tct	ctg	agc	att	ctg	ggg	aaa	aga	aac	tac	agt	
Thr	Pro	Asn	His	Thr	Ser	Leu	Ser	Ile	Leu	Gly	Lys	Arg	Asn	Tyr	Ser	
592				597					602				607			
cat	cac	aat	ggt	ctg	gat	gaa	ctc	acg	tgc	tgt	gtg	tca	gac	tga	gct	
His	His	Asn	Gly	Leu	Asp	Glu	Leu	Thr	Cys	Cys	Val	Ser	Asp	*		
608				613					618							2112
ttccctgatt cattctacaa tccaagactt gctgcactgt cctgctgatg ttcacagccg																2172
tgcctggaa gaaggcagcc ccactcccag tacatttcag tgggagacct ctgcgntgca																2232
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cccggggact gggagaacag gatagcagca ggagtcgggg ggccgcccga g atg ggg																177
																Met
																Gly
																1
aac act acc tcg tgc gtg tcg tcc agt ccc aag ctc cgg agg aat																
Asn	Thr	Ser	Cys	Cys	Val	Ser	Ser	Pro	Lys	Leu	Arg	Arg	Asn			225
3			8			13				18						
gcc cac tcc cgg ctg gag tcc tac cgg cca gac acg gac ctg agc cgc																
Ala	His	Ser	Arg	Leu	Glu	Ser	Tyr	Arg	Pro	Asp	Thr	Asp	Leu	Ser	Arg	
19			24			29				34						273
gag gac acg ggc tgc aac ctg cag cac atc agc gac cgg gag aac ata																
Glu	Asp	Thr	Gly	Cys	Asn	Leu	Gln	His	Ile	Ser	Asp	Arg	Glu	Asn	Ile	
35			40			45			50							321

gac gat ttg aac atg gaa ttc aat cct tca gat cat cct cg ^g gcc agc Asp Asp Leu Asn Met Glu Phe Asn Pro Ser Asp His Pro Arg Ala Ser 51 56 61 66	369
aca ata ttc ctc agt aaa tct cag aca gac gtg aga gaa aaa cgc aag Thr Ile Phe Leu Ser Lys Ser Gln Thr Asp Val Arg Glu Lys Arg Lys 67 72 77 82	417
agt ctc ttc att aac cat cat cct cca gga caa ata gca agg aaa tac Ser Leu Phe Ile Asn His His Pro Pro Gly Gln Ile Ala Arg Lys Tyr 83 88 93 98	465
agt tcc tgc tcc acc att ttc cta gat gat agc aca gtc agt caa cca Ser Ser Cys Ser Thr Ile Phe Leu Asp Asp Ser Thr Val Ser Gln Pro 99 104 109 114	513
aac ctc aag tat aca att aaa tgt gtc gct ctt gca ata tat tat cac Asn Leu Lys Tyr Thr Ile Lys Cys Val Ala Leu Ala Ile Tyr Tyr His 115 120 125 130	561
atc aaa aac agg gac cca gat gga agg atg ctc tta gat att ttt gat Ile Lys Asn Arg Asp Pro Asp Gly Arg Met Leu Leu Asp Ile Phe Asp 131 136 141 146	609
gaa aat ctt cac cct ctt tcg aaa tcc gaa gtg cca cca gat tat gac Glu Asn Leu His Pro Leu Ser Lys Ser Glu Val Pro Pro Asp Tyr Asp 147 152 157 162	657
aaa cac aac cca gag cag aag cag att tac cgg ttc gtt cgg aca ctg Lys His Asn Pro Glu Gln Lys Gln Ile Tyr Arg Phe Val Arg Thr Leu 163 168 173 178	705
ttc agt gct cag ctg acg gct gaa tgt gcc atc gtc acc ctg gtg Phe Ser Ala Ala Gln Leu Thr Ala Glu Cys Ala Ile Val Thr Leu Val 179 184 189 194	753
tac ctt gaa aga ctt tta aca tac gca gag ata gat atc tgt ccg gcc Tyr Leu Glu Arg Leu Leu Thr Tyr Ala Glu Ile Asp Ile Cys Pro Ala 195 200 205 210	801
aac tgg aag cgg att gtt tta ggg gcg atc ctg ctg gcc tcc aag gtg Asn Trp Lys Arg Ile Val Leu Gly Ala Ile Leu Leu Ala Ser Lys Val 211 216 221 226	849
tgg gat gac cag gct gta tgg aat gtg gat tac tgc cag atc ctg aaa Trp Asp Asp Gln Ala Val Trp Asn Val Asp Tyr Cys Gln Ile Leu Lys 227 232 237 242	897
gac atc acg gtg gag gac atg aac gag cta gag cga cag ttt ctt gaa Asp Ile Thr Val Glu Asp Met Asn Glu Leu Glu Arg Gln Phe Leu Glu 243 248 253 258	945
ttg ctg cag ttc aac atc aat gtt cct tcc agt gtc tat gcc aag tat Leu Leu Gln Phe Asn Ile Asn Val Pro Ser Ser Val Tyr Ala Lys Tyr 259 264 269 274	993

tat ttt gat ctt cgt tct ctg gca gaa gcg aac aac ctg agc ttt ccc 1041
 Tyr Phe Asp Leu Arg Ser Leu Ala Glu Ala Asn Asn Leu Ser Phe Pro
 275 280 285 290

 ttg gag ccc ctg agc agg gag agg gct cac aag ctt gag gcc atc tct 1089
 Leu Glu Pro Leu Ser Arg Glu Arg Ala His Lys Leu Glu Ala Ile Ser
 291 296 301 306

 cgc ctc tgc gag gac aag tac aag gac cta aga aga tcc gcg agg aag 1137
 Arg Leu Cys Glu Asp Lys Tyr Lys Asp Leu Arg Arg Ser Ala Arg Lys
 307 312 317 322

 cgc tca gcc agt gca gac aac ctg act ctg ccc cg^g tgg tcc cca gcc 1185
 Arg Ser Ala Ser Ala Asp Asn Leu Thr Leu Pro Arg Trp Ser Pro Ala
 323 328 333 338

 atc atc tct taa cta cggaggcccg ccggaggcca caccatccct tagttctcc 1240
 Ile Ile Ser *
 339

 tttagtttga gaaaagacag acttggggtg ggtttgttt tgttttttct ttcctttct 1300
 ttttttacgc atagctccgt caagctgcct ggatgagcgc ccatgcagca aggcttggag
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 tcctgtttaa cttcttgcatt tccttctgct gctttttgg gatggggta tttttgttca 1660
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tcagaccctt gtcatgcgc a ttgagagtcc tctagacagg cgctcctcgc agcaccgtag 180
tgcgc~~t~~tgcg ctgagcagcc cgcgaggcg gaagtggag ctgcgaccgc gctccctgtg 240
aggtggcaa gcggcgaat atg gcg ccc tcc ggg agt ctt gca gtt ccc ctg 291
Met Ala Pro Ser Gly Ser Leu Ala Val Pro Leu
1 5
gca gtc ctg gtg ctg ttg ctt tgg ggt gct ccc tgg acg cac ggg cgg 339
Ala Val Leu Val Leu Leu Leu Trp Gly Ala Pro Trp Thr His Gly Arg
12 17 22 27
cgg agc aac gtt cgc gtc atc acg gac gag aac tgg aga gaa ctg ctg 387
Arg Ser Asn Val Arg Val Ile Thr Asp Glu Asn Trp Arg Glu Leu Leu
28 33 38 43
gaa gga gac tgg atg ata gaa ttt tat gcc ccg tgg tgc cct gct tgt 435
Glu Gly Asp Trp Met Ile Glu Phe Tyr Ala Pro Trp Cys Pro Ala Cys
44 49 54 59
caa aat ctt caa ccg gaa tgg gaa agt ttt gct gaa tgg gga gaa gat 483
Gln Asn Leu Gln Pro Glu Trp Glu Ser Phe Ala Glu Trp Gly Glu Asp
60 65 70 75
ctt gag gtt aat att gcg aaa gta gat gtc aca gag cag cca gga ctg 531
Leu Glu Val Asn Ile Ala Lys Val Asp Val Thr Glu Gln Pro Gly Leu
76 81 86 91
agt gga cgg ttt atc ata act gct ctt cct act att tat cat tgt aaa 579
Ser Gly Arg Phe Ile Ile Thr Ala Leu Pro Thr Ile Tyr His Cys Lys
92 97 102 107
gat ggt gaa ttt agg cgc tat cag ggt cca agg act aag aag gac ttc 627
Asp Gly Glu Phe Arg Arg Tyr Gln Gly Pro Arg Thr Lys Lys Asp Phe
108 113 118 123
ata aac ttt ata agt gat aaa gag tgg aag agt att gag ccc gtt tca 675
Ile Asn Phe Ile Ser Asp Lys Glu Trp Lys Ser Ile Glu Pro Val Ser
124 129 134 139
tca tgg ttt ggt cca ggt tct gtt ctg atg agt agt atg tca gca ctc 723
Ser Trp Phe Gly Pro Gly Ser Val Leu Met Ser Ser Met Ser Ala Leu
140 145 150 155

ttt cag cta tct atg tgg atc agg acg tgc cat aac tac ttt att gaa Phe Gln Leu Ser Met Trp Ile Arg Thr Cys His Asn Tyr Phe Ile Glu	156	161	166	171	771
gac ctt gga ttg cca gtg tgg gga tca tat act gtt ttt gct tta gca Asp Leu Gly Leu Pro Val Trp Gly Ser Tyr Thr Val Phe Ala Leu Ala	172	177	182	187	819
act ctg ttt tcc gga ctg tta gga ctc tgt atg ata ttt gtg gca Thr Leu Phe Ser Gly Leu Leu Leu Gly Leu Cys Met Ile Phe Val Ala	188	193	198	203	867
gat tgc ctt tgt cct tca aaa agg cgc aga cca cag cca tac cca tac Asp Cys Leu Cys Pro Ser Lys Arg Arg Arg Pro Gln Pro Tyr Pro Tyr	204	209	214	219	915
cct tca aaa aaa tta tta tca gaa tct gca caa cct ttg aaa aaa gtg Pro Ser Lys Lys Leu Leu Ser Glu Ser Ala Gln Pro Leu Lys Lys Val	220	225	230	235	963
gag gag gaa caa gag gcg gat gaa gaa gat gtt tca gaa gaa gaa gct Glu Glu Glu Gln Glu Ala Asp Glu Glu Asp Val Ser Glu Glu Glu Ala	236	241	246	251	1011
gaa agt aaa gaa gga aca aac aaa gac ttt cca cag aat gcc ata aga Glu Ser Lys Glu Gly Thr Asn Lys Asp Phe Pro Gln Asn Ala Ile Arg	252	257	262	267	1059
caa cgc tct ctg ggt cca tca ttg gcc aca gat aaa tcc tag ttaaatt Gln Arg Ser Leu Gly Pro Ser Leu Ala Thr Asp Phe Pro Gln Asn Ala Ile Arg	268	273	278		1108
ttatagttat ctttatattat tgattttgat aaaaacagaa gattgatcat ttgttttgtt					1168
ttgaagtgaa ctgtgacttt ttgttatatt gcagggttca gtctagattt tcattaaatt					1228
gaagagtcta cattcagaac ataaaaagcac taggtataca agttgaaat atgatttaag					1288
cacagtatga tggtttaaat agttctctaa ttttgaaaa atcgtgccaa gcaataagat					1348
ttatgtatat ttgtttataataaacattt tcaagtctga gtttgaaaa ttacatttc					1408
ccaagtattt cattatttagag gtatttaaga agattatttt agagaaaaat atttctcatt					1468
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agtttgccca ttgtctcaag aaatgtgtat ttcaagtaca atttcgttgtt ctttttagag					1588
gtatattcca aaatttcctt gtattttag gttatgcaac taataaaaac taccttacat					1648
taattaatta cagtttctta cacatggtaa tacaggatat gctactgatt taggaagttt					1708
ttaagttcat ggtattctct tgattccaac aaagttgtat ttctcttgtt atttttctta					1768
cttactatgg gttacatttt ttattttca aattggatga taatttcttg gaaacatttt					1828

ttatgttta gtaaacagta ttttcttgg ttttcaact gaagttact gagagatcca 1888
 tcaaattgaa caatctgtt taatttaaaa ttttggccac tttttcaga ttttacatca 1948
 ttcttgctga acttcaactt gaaattgtt tttttttt ttcttttgg atgtgaaggt 2008
 gaacattcct gatTTTgtc tgatgtgaaa aagccttggt atttacatt ttgaaaattc 2068
 aaagaagctt aatataaaaag tttgcattct actcaggaaa aagcatcttc ttgtatatgt 2128
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 ggaacattttt agtgtatTTT tactccttaa agagctagaa tacatagttt tcaccttaaa 2368
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 gtaatgtccc cttcttcta ggctctgtt ctgtgtgaat ccattagatt tacagtatcg 2488
 taatatacaa gtttcttta aagccctctc ctttagaatt taaaatattt accattgaa 2548
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	Met Ala Glu Glu Glu Ala	
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gcc aag ttg gag aag cac ttg atg ctt ctg cg	cag gag tat gtc aag	101
Ala Lys Leu Glu Lys His Leu Met Leu Leu Arg Gln Glu Tyr Val Lys		
7 12 17 22		

ctg caa aag aag ctg gcg gag aca gag aag cgc tgc gct ctc ttg gct	/	149
Leu Gln Lys Lys Leu Ala Glu Thr Glu Lys Arg Cys Ala Leu Leu Ala		
23 28 33 38		

gcg cag gca aac aag gag agc agc gag tcc ttc atc agc cgt ctg Ala Gln Ala Asn Lys Glu Ser Ser Ser Glu Ser Phe Ile Ser Arg Leu	197
39 44 49 54	
 ctg gcc atc gtg gca gac ctc tac gag cag gag cag tac agc gat ctg Leu Ala Ile Val Ala Asp Leu Tyr Glu Gln Glu Gln Tyr Ser Asp Leu	245
55 60 65 70	
 aag ata aag gtt ggg gac agg cac atc agt gct cac aag ttt gtc ctg Lys Ile Lys Val Gly Asp Arg His Ile Ser Ala His Lys Phe Val Leu	293
71 76 81 86	
 tca gcc cgc agt gac agc tgg agt ctg gct aac ttg tct tcc act aaa Ser Ala Arg Ser Asp Ser Trp Ser Leu Ala Asn Leu Ser Ser Thr Lys	341
87 92 97 102	
 gag ttg gac ctg tca gat gct aat cct gag gtg acg atg aca atg ctt Glu Leu Asp Leu Ser Asp Ala Asn Pro Glu Val Thr Met Thr Met Leu	389
103 108 113 118	
 cgc tgg atc tat aca gat gag ctg gag ttc aga gag gat gat gtg ttc Arg Trp Ile Tyr Thr Asp Glu Leu Glu Phe Arg Glu Asp Asp Val Phe	437
119 124 129 134	
 ctg act gaa ctg atg aaa cta gca aat cgg ttt cag cta cag ctc ctc Leu Thr Glu Leu Met Lys Leu Ala Asn Arg Phe Gln Leu Gln Leu Leu	485
135 140 145 150	
 agg gag aga tgt gag aag ggt gtt atg tct cta gtg aat gtc agg aac Arg Glu Arg Cys Glu Lys Gly Val Met Ser Leu Val Asn Val Arg Asn	533
151 156 161 166	
 tgt att cgc ttc tac cag acg gca gag gag ctg aat gcc agc aca ctg Cys Ile Arg Phe Tyr Gln Thr Ala Glu Glu Leu Asn Ala Ser Thr Leu	581
167 172 177 182	
 atg aac tac tgt gca gaa att att gca agt cat tgg gac gac ctg agg Met Asn Tyr Cys Ala Glu Ile Ile Ala Ser His Trp Asp Asp Leu Arg	629
183 188 193 198	
 aag gag gat ttc agc agc atg agc cct cag ttg tta tac aaa atg atc Lys Glu Asp Phe Ser Ser Met Ser Pro Gln Leu Leu Tyr Lys Met Ile	677
199 204 209 214	
 aaa tcc aag aca gag tac ccg cta cat aaa gcc atc aaa gtg gag aga Lys Ser Lys Thr Glu Tyr Pro Leu His Lys Ala Ile Lys Val Glu Arg	725
215 220 225 230	
 gaa gac gtg gtc tcc ctg tat ctg att gaa atg gat tcc cag ctc cct Glu Asp Val Val Ser Leu Tyr Leu Ile Glu Met Asp Ser Gln Leu Pro	773
231 236 241 246	
 ggg aag ctg aat gaa gca gac cat aac ggg gac ctg gca tta gac cta Gly Lys Leu Asn Glu Ala Asp His Asn Gly Asp Leu Ala Leu Asp Leu	821
247 252 257 262	

gcc ctc tca cga cga ctg gag aat att	gcc acc acg ctg gtt agt cac	869
Ala Leu Ser Arg Arg Leu Glu Asn Ile Ala Thr Thr Leu Val Ser His		
263 268 273 278		
aaa gct gat gtg gac atg gtg gac aag agt	ggc tgg agc ttg tta cac	917
Lys Ala Asp Val Asp Met Val Asp Lys Ser Gly Trp Ser Leu Leu His		
279 284 289 294		
aaa gga atc caa aga gga gat ctc ttt gct	gcc act ttc ctc att aag	965
Lys Gly Ile Gln Arg Gly Asp Leu Phe Ala Ala Thr Phe Leu Ile Lys		
295 300 305 310		
aat ggg gcc ttt gtc aac gct gca ctg ggt	gcc cag gag aca cca	1013
Asn Gly Ala Phe Val Asn Ala Ala Thr Leu Gly Ala Gln Glu Thr Pro		
311 316 321 326		
ctg cac ctt gtg gcc ttg tac agt tca aag	aaa cac tca gca gat gtg	1061
Leu His Leu Val Ala Leu Tyr Ser Ser Lys Lys His Ser Ala Asp Val		
327 332 337 342		
atg tct gag atg gcg cag att gca gag gcc ctt	ctg cag gct ggt gcc	1109
Met Ser Glu Met Ala Gln Ile Ala Glu Ala Leu Leu Gln Ala Gly Ala		
343 348 353 358		
aac ccc aac atg cag gac aag ggg agg act	cct tta cat gtg tcc	1157
Asn Pro Asn Met Gln Asp Ser Lys Gly Arg Thr Pro Leu His Val Ser		
359 364 369 374		
atc atg gcc ggg aat gaa tat gtg ttc agt	cag ctg ctg cag tgc aaa	1205
Ile Met Ala Gly Asn Glu Tyr Val Phe Ser Gln Leu Leu Gln Cys Lys		
375 380 385 390		
caa cta gat tta gaa ctc aaa gac cac gag	ggc agc acg gct ctg tgg	1253
Gln Leu Asp Leu Glu Leu Lys Asp His Glu Gly Ser Thr Ala Leu Trp		
391 396 401 406		
ctg gca gtg cag cat atc aca gtg tct tct	gac cag tct gtg aac ccc	1301
Leu Ala Val Gln His Ile Thr Val Ser Ser Asp Gln Ser Val Asn Pro		
407 412 417 422		
tcc gaa gat gtc ccc gtg gta aat ggg act	tca ttt gat gag aac agc	1349
Phe Glu Asp Val Pro Val Val Asn Gly Thr Ser Phe Asp Glu Asn Ser		
423 428 433 438		
ttt gca gcc aga ctc atc cag cgc ggc agc	cac aca gac gca cct gac	1397
Phe Ala Ala Arg Leu Ile Gln Arg Gly Ser His Thr Asp Ala Pro Asp		
439 444 449 454		
acg gcg aca gga aac tgt tta cta cag cgg	gca gct gga gca gga aac	1445
Thr Ala Thr Gly Asn Cys Leu Leu Gln Arg Ala Ala Gly Ala Gly Asn		
455 460 465 470		
gag gca gca gct ctt ttc ctg gca acc aac	ggt gcc cat gtc aac cac	1493
Glu Ala Ala Ala Leu Phe Leu Ala Thr Asn Gly Ala His Val Asn His		
471 476 481 486		
aga aac aag tgg gga gaa acc ccg ttg cac	aca gcg tgt cgg cat ggc	1541

Arg Asn Lys Trp Gly Glu Thr Pro Leu His Thr Ala Cys Arg His Gly			
487	492	497	502
ctg gcc aac ctc aca gca gag ctc ctg cag caa ggc gcc aac cca aac			1589
Leu Ala Asn Leu Thr Ala Glu Leu Leu Gln Gln Gly Ala Asn Pro Asn			
503	508	513	518
ctg cag acg gag gaa gct ctg cct ctg cca aag gag gcc gca tcc ctg			1637
Leu Gln Thr Glu Ala Leu Pro Leu Pro Lys Glu Ala Ala Ser Leu			
519	524	529	534
acc agc ttg gcg gac agc gtc cat ctg cag acg cca ctg cac atg gcg			1685
Thr Ser Leu Ala Asp Ser Val His Leu Gln Thr Pro Leu His Met Ala			
535	540	545	550
atc gcc tat aac cat ccg gat gtg gtg tct gtc atc ctg gag cag aaa			1733
Ile Ala Tyr Asn His Pro Asp Val Val Ser Val Ile Leu Glu Gln Lys			
551	556	561	566
gcc aat gct ctt cat gcc acc aac aac ttg cag atc att ccg gac ttc			1781
Ala Asn Ala Leu His Ala Thr Asn Asn Leu Gln Ile Ile Pro Asp Phe			
567	572	577	582
agc ctc aaa gat tcc cga gac cag act gtg ctg ggc ctg gca tta tgg			1829
Ser Leu Lys Asp Ser Arg Asp Gln Thr Val Leu Gly Leu Ala Leu Trp			
583	588	593	598
act ggc atg cac acg atc gca gcc cag ctg ctg ggc tct gga gcc gcc			1877
Thr Gly Met His Thr Ile Ala Ala Gln Leu Leu Gly Ser Gly Ala Ala			
599	604	609	614
atc aat gac acc atg tcg gat ggg cag acg cta ctg cac atg gcc ata			1925
Ile Asn Asp Thr Met Ser Asp Gly Gln Thr Leu Leu His Met Ala Ile			
615	620	625	630
cag cgg cag gac agc aag agc gca ctc ttc ctg ctg gag cac cag gca			1973
Gln Arg Gln Asp Ser Lys Ser Ala Leu Phe Leu Leu Glu His Gln Ala			
631	636	641	646
gat ata aat gtc agc agg act cag gac ggg gag aca gcc ctc cag ctg			2021
Asp Ile Asn Val Ser Arg Thr Gln Asp Gly Glu Thr Ala Leu Gln Leu			
647	652	657	662
gcc atc aga aac cag ctt cca ctc gta gtt gat gcc ata tgc acc cga			2069
Ala Ile Arg Asn Gln Leu Pro Leu Val Val Asp Ala Ile Cys Thr Arg			
663	668	673	678
gga gct gac atg tct gtg cca gat gag aag ggg aac ccc ccg ctg tgg			2117
Gly Ala Asp Met Ser Val Pro Asp Glu Lys Gly Asn Pro Pro Leu Trp			
679	684	689	694
ctt gca ttg gca aac aat ctg gag gac atc gca tcc act ctg gtc aga			2165
Leu Ala Leu Ala Asn Asn Leu Glu Asp Ile Ala Ser Thr Leu Val Arg			
695	700	705	710
cat ggc tgt gat gcc aca tgc tgg ggt ccg gga cct ggt ggg tgc ctt			2213
His Gly Cys Asp Ala Thr Cys Trp Gly Pro Gly Pro Gly Cys Leu			

711	716	721	726	
cag acg ctc ctg cac aga gcc att gat gaa aac aac gag ccc acc gcc Gln Thr Leu Leu His Arg Ala Ile Asp Glu Asn Asn Glu Pro Thr Ala				2261
727	732	737	742	
tgc ttt ctt att cgc agt ggc tgt gac gtg aac agt ccc aga caa cca Cys Phe Leu Ile Arg Ser Gly Cys Asp Val Asn Ser Pro Arg Gln Pro				2309
743	748	753	758	
ggc gcc aat gga gaa gga gag gaa gag gct aga gat ggg cag acc cct Gly Ala Asn Gly Gly Glu Glu Ala Arg Asp Gly Gln Thr Pro				2357
759	764	769	774	
ttg cat ttg gca gcc tct tgg ggg ctg gaa gag aca gta cag tgt ctt Leu His Leu Ala Ala Ser Trp Gly Leu Glu Glu Thr Val Gln Cys Leu				2405
775	780	785	790	
ctg gag ttt ggt gcc aac gtg aac gca cag gat gca gaa gga aga acc Leu Glu Phe Gly Ala Asn Val Asn Ala Gln Asp Ala Glu Gly Arg Thr				2453
791	796	801	806	
ccc atc cac gtg gcc atc agc agc caa cac ggt gtc atc att cag ctg Pro Ile His Val Ala Ile Ser Ser Gln His Gly Val Ile Ile Gln Leu				2501
807	812	817	822	
ttg gtt tct cac ccc gat atc cat ttg aat gta cgg gac aga caa ggg Leu Val Ser His Pro Asp Ile His Leu Asn Val Arg Asp Arg Gln Gly				2549
823	828	833	838	
ctg acc ccg ttt gcc tgt gcc atg act ttc aag aac aac aag tca gcc Leu Thr Pro Phe Ala Cys Ala Met Thr Phe Lys Asn Asn Lys Ser Ala				2597
839	844	849	854	
gag gcc att ctc aaa cga gag tca ggg gct gct gag cag gtg gat aac Glu Ala Ile Leu Lys Arg Glu Ser Gly Ala Ala Glu Gln Val Asp Asn				2645
855	860	865	870	
aag ggc cgg aat ttc ctt cat gtg gca gtt cag aac tct gat att gaa Lys Gly Arg Asn Phe Leu His Val Ala Val Gln Asn Ser Asp Ile Glu				2693
871	876	881	886	
agt gtg ctg ttc ctg atc agt gtc cac gct aat gtg aat tca aga gtc Ser Val Leu Phe Leu Ile Ser Val His Ala Asn Val Asn Ser Arg Val				2741
887	892	897	902	
cag gat gcc tcc aag ttg acc ccc ctg cac ctc gct gtc caa gca ggc Gln Asp Ala Ser Lys Leu Thr Pro Leu His Leu Ala Val Gln Ala Gly				2789
903	908	913	918	
tca gaa att att gtc cgc aat ttg ctt ctt gcg gga gcc aaa gtg aac Ser Glu Ile Ile Val Arg Asn Leu Leu Leu Ala Gly Ala Lys Val Asn				2837
919	924	929	934	
gaa tta act aag cat cgc cag act gcc ctc cat ctt gct gcc cag cag Glu Leu Thr Lys His Arg Gln Thr Ala Leu His Leu Ala Ala Gln Gln				2885
935	940	945	950	

gac ctg ccc acc atc tgc tca gtc ctc cta gag aat ggc gtg gac ttt		2933
Asp Leu Pro Thr Ile Cys Ser Val Leu Leu Glu Asn Gly Val Asp Phe		
951 956 961 966		
gct gcc gtg gat gag aat gga aac aat gct ctt cat ctt gct gtc atg		2981
Ala Ala Val Asp Glu Asn Gly Asn Asn Ala Leu His Leu Ala Val Met		
967 972 977 982		
cac ggc cggtt ctc aac aac atc cggtt ctc ctg aca gag tgc aca gtg		3029
His Gly Arg Leu Asn Asn Ile Arg Val Leu Leu Thr Glu Cys Thr Val		
983 988 993 998		
gac gcc gaa gcc ttt aat ctc aga ggc cag tca ccatttg cac att ttg		3077
Asp Ala Glu Ala Phe Asn Leu Arg Gly Gln Ser Pro Leu His Ile Leu		
999 1004 1009 1014		
gga caa tat ggc aag gag aat gca gcg gcc atc ttt gat ctc ttc cta		3125
Gly Gln Tyr Gly Lys Glu Asn Ala Ala Ile Phe Asp Leu Phe Leu		
1015 1020 1025 1030		
gaa tgc atg ccg ggg tat cct ctg gac aag ccg gat gca gac ggc agc		3173
Glu Cys Met Pro Gly Tyr Pro Leu Asp Lys Pro Asp Ala Asp Gly Ser		
1031 1036 1041 1046		
acg gtg ctg ctc ctg gca tac atg aaa ggg aac gcc aac ttg tgc cgc		3221
Thr Val Leu Leu Ala Tyr Met Lys Gly Asn Ala Asn Leu Cys Arg		
1047 1052 1057 1062		
gcc atc gtc cggtt ggg gct cgc ctc ggg gtg aat aac aac cag gga		3269
Ala Ile Val Arg Ser Gly Ala Arg Leu Gly Val Asn Asn Gln Gly		
1063 1068 1073 1078		
gtc aac atc ttc aac tac cag gtc gcc acc aag cag ctc ctg ttc cga		3317
Val Asn Ile Phe Asn Tyr Gln Val Ala Thr Lys Gln Leu Leu Phe Arg		
1079 1084 1089 1094		
ctg ctg gat atg ctg tcc aag gag cct ccg tgg tgt gac ggc tcc tac		3365
Leu Leu Asp Met Leu Ser Lys Glu Pro Pro Trp Cys Asp Gly Ser Tyr		
1095 1100 1105 1110		
tgc tat gag tgc act gcc agg ttc gga gtc acc act cgc aaa cac cac		3413
Cys Tyr Glu Cys Thr Ala Arg Phe Gly Val Thr Thr Arg Lys His His		
1111 1116 1121 1126		
tgt cgt cac tgc gga cgt ctt ctt tgc cat aaa tgc tgc acc aag gag		3461
Cys Arg His Cys Gly Arg Leu Leu Cys His Lys Cys Ser Thr Lys Glu		
1127 1132 1137 1142		
att cct att ata aag ttt gat ctg aac aag cct gtg ccg gtt tgc aac		3509
Ile Pro Ile Ile Lys Phe Asp Leu Asn Lys Pro Val Arg Val Cys Asn		
1143 1148 1153 1158		
att tgt ttt gat gta ctg act ctg ggt ggg gtt tct tag tgagcccccc		3558
Ile Cys Phe Asp Val Leu Thr Leu Gly Gly Val Ser *		
1159 1164 1169		

ggagggtcca ggccacgtcc ttggtcacct ccccagcagc tgctctgctc accagcctga	3618
ccccacccag agcaggagct ggcgggtgtc ttcctgcggc aatagactgg aacgattaag	3678
gaccatggtg tgatagatcc catttcaa at gattccat at gattgtca gtgtgctgtc	3738
agactgtgat cgatttca ct agatgtctca ctc atc agan caggcattcg ggctaagtgg	3798
taaatgtgat taggaatnag acctcctccc attctgctag caacatacag ggacacttgg	3858
aaaaccattt cccttccagt cagcttggtg tccatcccc gagccaattt caatggaaan	3918
gcctttccc ccggccccctt ggggggcctg gacctgatng agcgcagagc ctctcagcgt	3978
aggaagctgg ctgcttaatc gagctggctt tactcttaggg taagtggctg tggactttc	4038
tgcacagtgt tttcataaaag ataataggat cctcttgccct gaagtctttt tttctttta	4098
cg	4100

<210> 1072
 <211> 777
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (36) .. (653)

<400> 1072

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	Met Ala Glu Glu Glu Ala	
	1	

gcc aag ttg gag aag cac ttg atg ctt ctg cgg cag gag tat gtc aag	101
Ala Lys Leu Glu Lys His Leu Met Leu Leu Arg Gln Glu Tyr Val Lys	
7 12 17 22	

ctg caa aag aag ctg gcg gag aca gag aag cgc tgc gct ctc ttg gct	149
Leu Gln Lys Lys Leu Ala Glu Thr Glu Lys Arg Cys Ala Leu Leu Ala	
23 28 33 38	

gcg cag gca aac aag gag agc agc gag tcc ttc atc agc cgt ctg	197
Ala Gln Ala Asn Lys Glu Ser Ser Glu Ser Phe Ile Ser Arg Leu	
39 44 49 54	

ctg gcc atc gtg gca gac ctc tac gag cag gag cag tac agc gat ctg	245
Leu Ala Ile Val Ala Asp Leu Tyr Glu Gln Glu Gln Tyr Ser Asp Leu	
55 60 65 70	

aag ata aag gtt ggg gac agg cac atc agt gct cac aag ttt gtc ctg	293
Lys Ile Lys Val Gly Asp Arg His Ile Ser Ala His Lys Phe Val Leu	
71 76 81 86	

tca	gcc	cgc	agt	gac	agc	tgg	agt	ctg	gct	aac	ttg	tct	tcc	act	aaa	341
Ser	Ala	Arg	Ser	Asp	Ser	Trp	Ser	Leu	Ala	Asn	Leu	Ser	Ser	Thr	Lys	
87				92					97					102		
gag	ttg	gac	ctg	tca	gat	gct	aat	cct	gag	gtg	acg	atg	aca	atg	ctt	389
Glu	Leu	Asp	Leu	Ser	Asp	Ala	Asn	Pro	Glu	Val	Thr	Met	Thr	Met	Leu	
103				108				113				118				
cgc	tgg	atc	tat	aca	gat	gag	ctg	gag	ttc	aga	gag	gat	gat	gtg	ttc	437
Arg	Trp	Ile	Tyr	Thr	Asp	Glu	Leu	Glu	Phe	Arg	Glu	Asp	Asp	Val	Phe	
119				124					129				134			
ctg	act	gaa	ctg	atg	aaa	cta	gca	aat	cgg	ttt	cag	cta	cag	ctc	ctc	485
Leu	Thr	Glu	Leu	Met	Lys	Leu	Ala	Asn	Arg	Phe	Gln	Leu	Gln	Leu	Leu	
135				140					145				150			
agg	gag	aga	tgt	gag	aag	ggt	gtt	atg	tct	cta	gtg	aat	gtc	agg	aac	533
Arg	Glu	Arg	Cys	Glu	Lys	Gly	Val	Met	Ser	Leu	Val	Asn	Val	Arg	Asn	
151				156				161					166			
tgt	att	cgc	ttc	tac	cag	acg	gca	gag	gag	ctg	aat	gcc	agc	aca	ctg	581
Cys	Ile	Arg	Phe	Tyr	Gln	Thr	Ala	Glu	Glu	Leu	Asn	Ala	Ser	Thr	Leu	
167				172					177				182			
atg	aac	tac	tgt	gca	gaa	att	att	gca	agt	cat	tgg	gtg	agt	gag	gtt	629
Met	Asn	Tyr	Cys	Ala	Glu	Ile	Ile	Ala	Ser	His	Trp	Val	Ser	Glu	Val	
183				188					193				198			
gag	ggt	gtc	aac	aaa	gca	ctc	tag	ctggcagtca	ggagaccgcc	gctggggacg						683
Glu	Gly	Val	Asn	Lys	Ala	Leu	*									
199				204												
tagttccatg	gaaaagtgacc	tctctggcac	ctggttttct	cttgttacac	aattgaagaa											743
taaatagttt	aaaaaagatga	aaaaaaaaaaa	aaaa													777

<210> 1073
 <211> 1635
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (92)..(1090)

<400> 1073

agctggacga ggacaggcggtt gtcggccgc ccgtaagatgtctgtaccccttgaccctgc 60

cgttcagctc tagggccccgt gcaggcacac c atg aac acc tcc cca ggc acg 112
Met Asn Thr Ser Pro Gly Thr
1 / 5

gtg ggc agt gac ccg gtc atc ctg gcc act gca ggc tac gac cac acc 160
Val Gly Ser Asp Pro Val Ile Leu Ala Thr Ala Gly Tyr Asp His Thr

8	13	18	23	
gtg cgc ttc tgg cag gcc cac agc ggc atc tgc acc cgg acg gtg cag Val Arg Phe Trp Gln Ala His Ser Gly Ile Cys Thr Arg Thr Val Gln	24	29	34	208
24	29	34	39	
cac cag gac tcc cag gtg aat gcc ttg gag gtc aca ccg gac cgc acg His Gln Asp Ser Gln Val Asn Ala Leu Glu Val Thr Pro Asp Arg Ser	40	45	50	256
40	45	50	55	
atg att gct gct gca gtt cag cct gtg tcc cta ggt tac cag cac atc Met Ile Ala Ala Ala Val Gln Pro Val Ser Leu Gly Tyr Gln His Ile	56	61	66	304
56	61	66	71	
cgc atg tat gat ctc aac tcc aat aac cct aac ccc atc atc agc tac Arg Met Tyr Asp Leu Asn Ser Asn Asn Pro Asn Pro Ile Ile Ser Tyr	72	77	82	352
72	77	82	87	
gac ggc gtc aac aag aac atc gcg tct gtg ggc ttc cac gaa gac ggc Asp Gly Val Asn Lys Asn Ile Ala Ser Val Gly Phe His Glu Asp Gly	88	93	98	400
88	93	98	103	
cgc tgg atg tac acg ggc ggc gag gac tgc aca gcc agg atc tgg gac Arg Trp Met Tyr Thr Gly Gly Glu Asp Cys Thr Ala Arg Ile Trp Asp	104	109	114	448
104	109	114	119	
ctc agg tcc cgg aac ctg cag tgc cag cgg atc ttc cag gtg aac gca Leu Arg Ser Arg Asn Leu Gln Cys Gln Arg Ile Phe Gln Val Asn Ala	120	125	130	496
120	125	130	135	
ccc att aac tgc gtg tgc ctg cac ccc aac cag gca gag ctc atc gtg Pro Ile Asn Cys Val Cys Leu His Pro Asn Gln Ala Glu Leu Ile Val	136	141	146	544
136	141	146	151	
ggt gac cag agc ggg gct atc cac atc tgg gac ttg aaa aca gac cac Gly Asp Gln Ser Gly Ala Ile His Ile Trp Asp Leu Lys Thr Asp His	152	157	162	592
152	157	162	167	
aac gag cag ctg atc cct gag ccc gag gtc tcc atc acg tcc gcc cac Asn Glu Gln Leu Ile Pro Glu Pro Glu Val Ser Ile Thr Ser Ala His	168	173	178	640
168	173	178	183	
atc gat ccc gac gcc agc tac atg gca gct gtc aat agc acc gga aac Ile Asp Pro Asp Ala Ser Tyr Met Ala Ala Val Asn Ser Thr Gly Asn	184	189	194	688
184	189	194	199	
tgc tat gtc tgg aat ctg acg ggg ggc att ggt gac gag gtg acc cag Cys Tyr Val Trp Asn Leu Thr Gly Gly Ile Gly Asp Glu Val Thr Gln	200	205	210	736
200	205	210	215	
ctc atc ccc aag act aag atc cct gcc cac acg cgc tac gcc ctg cag Leu Ile Pro Lys Thr Lys Ile Pro Ala His Thr Arg Tyr Ala Leu Gln	216	221	226	784
216	221	226	231	
tgt cgc ttc agc ccc gac tcc acg ctc ctc gcc acc tgc tcg gct gat Cys Arg Phe Ser Pro Asp Ser Thr Leu Leu Ala Thr Cys Ser Ala Asp	232	237	242	832
232	237	242	247	

cag acg tgc aag atc tgg agg acg tcc aac ttc tcc ctg atg acg gag Gln Thr Cys Lys Ile Trp Arg Thr Ser Asn Phe Ser Leu Met Thr Glu 248 253 258 263	880
ctg agc atc aag agc ggc aac ccc ggg gag tcc tcc cgc ggc tgg atg Leu Ser Ile Lys Ser Gly Asn Pro Gly Glu Ser Ser Arg Gly Trp Met 264 269 274 279	928
tgg ggc tgc gcc ttc tcg ggg gac tcc cag tac atc gtc act gct tcc Trp Gly Cys Ala Phe Ser Gly Asp Ser Gln Tyr Ile Val Thr Ala Ser 280 285 290 295	976
tcg gac aac ctg gcc cgg ctc tgg tgt gtg gag act gga gag atc aag Ser Asp Asn Leu Ala Arg Leu Trp Cys Val Glu Thr Gly Glu Ile Lys 296 301 306 311	1024
aga gag tat ggc ggc cac cag aag gct gtt gtc tgc ctg gcc ttc aat Arg Glu Tyr Gly His Gln Lys Ala Val Val Cys Leu Ala Phe Asn 312 317 322 327	1072
gac agt gtg ctg ggc tag cctgtg acccctcgaa actgcctggc gcaggtggc Asp Ser Val Leu Gly * 328 333	1126
gcagctggag ggaccatgc agcacccagg tcagagcaga ccctccccctg ccggcctgcg ccagctggac ctgatggccc cctgtggcgc cttgacctgc tggccagggc tgccctggaa ctctcagccc ccagttgtt atccagatgt gacagagctc gacccaagcc aggctgcaca ctcctggact gggcttagcct gcactgcctg ggaaagtccg ccgagggccc aaagctgctg aggggtctga ggctggtgcc caccccaag ctatgtgtt ctctgccct ccctgcccgc gtttcagggc ctccgtccat agagaacacc accaccatgg ccaggtggaa gggtttatta gtccctgcca gcagctgtcc tccctggcgc aggtggcctg gccagccac tggattgggg acggggccagg ctggggccagg tcgggggctc agtctggag gtaataaaag cagaccgaca cgccatgtt gtcggaaa aaaaaaaaaa 1635	1186 1246 1306 1366 1426 1486 1546 1606

<210> 1074
<211> 1755
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (128)..(1210)

<400> 1074

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60

cgcggccgta	agatgctctg	acctttgacc	cctgccgttc	agctctaggg	cccgtgcagg	120
ccacacc	atg aac acc tcc cca ggc acg gtg ggc agt gac ccg gtc atc					169
	Met Asn Thr Ser Pro Gly Thr Val Gly Ser Asp Pro Val Ile					
1	5			10		
ctg gcc act gca ggc tac gac cac acc gtg cgc ttc tgg cag gcc cac						217
Leu Ala Thr Ala Gly Tyr Asp His Thr Val Arg Phe Trp Gln Ala His						
15	20		25		30	
agc ggc atc tgc acc cgg acg gtg cag cac cag gac tcc cag gtg aat						265
Ser Gly Ile Cys Thr Arg Thr Val Gln His Gln Asp Ser Gln Val Asn						
31	36		41		46	
gcc ttg gag gtc aca ccg gac cgc agc atg att gct gct gca ggt tac						313
Ala Leu Glu Val Thr Pro Asp Arg Ser Met Ile Ala Ala Ala Gly Tyr						
47	52		57		62	
cag cac atc cgc atg tat gat ctc aac tcc aat aac cct aac ccc atc						361
Gln His Ile Arg Met Tyr Asp Leu Asn Ser Asn Asn Pro Asn Pro Ile						
63	68		73		78	
atc agc tac gac ggc gtc aac aag aac atc gcg tct gtg ggc ttc cac						409
Ile Ser Tyr Asp Gly Val Asn Lys Asn Ile Ala Ser Val Gly Phe His						
79	84		89		94	
gaa gac ggc cgc tgg atg tac acg ggc gag gac tgc aca gcc agg						457
Glu Asp Gly Arg Trp Met Tyr Thr Gly Gly Glu Asp Cys Thr Ala Arg						
95	100		105		110	
atc tgg gac ctc agg tcc cgg aac ctg cag tgc cag cgg atc ttc cag						505
Ile Trp Asp Leu Arg Ser Arg Asn Leu Gln Cys Gln Arg Ile Phe Gln						
111	116		121		126	
gtg aac gca ccc att aac tgc gtg tgc ctg cac ccg aac cag gca gag						553
Val Asn Ala Pro Ile Asn Cys Val Cys Leu His Pro Asn Gln Ala Glu						
127	132		137		142	
ctc atc gtg ggt gac cag acg ggg gct atc cac atc tgg gac ttg aaa						601
Leu Ile Val Gly Asp Gln Ser Gly Ala Ile His Ile Trp Asp Leu Lys						
143	148		153		158	
aca gac cac aac gag cag ctg atc cct gag ccc gag gtc tcc atc acg						649
Thr Asp His Asn Glu Gln Leu Ile Pro Glu Pro Glu Val Ser Ile Thr						
159	164		169		174	
tcc gcc cac atc gat ccc gac gcc agc tac atg gca gct gtc aat agc						697
Ser Ala His Ile Asp Pro Asp Ala Ser Tyr Met Ala Ala Val Asn Ser						
175	180		185		190	
acc ctg gtg ccc ttc tcc tgt cta ctt ccg ttg gcc atc ggc atc ctc						745
Thr Leu Val Pro Phe Ser Cys Leu Leu Pro Leu Ala Ile Gly Ile Leu						
191	196		201		206	
cag gaa gga gaa ttt gag tcc ttg gcc agg cgt ggc ctc ctg ttc ttg						793
Gln Glu Gly Glu Phe Glu Ser Leu Ala Arg Arg Gly Leu Leu Phe Leu						

<210> 1075

<211> 577

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (12)..(443)

<400> 1075

gaattcccg g atg cac agt acc cag gac aaa tct ctc cac ttg gaa gga	50
Met His Ser Thr Gln Asp Lys Ser Leu His Leu Glu Gly	
1 5 10	
gat ccc aat cct tct gca gcc cca aca tcc acc tgc gca cct agg aaa	98
Asp Pro Asn Pro Ser Ala Ala Pro Thr Ser Thr Cys Ala Pro Arg Lys	
14 19 24 29	
atg ccc aaa agg att tca ata tcc aaa caa ctg gct tca gtg aaa gct	146
Met Pro Lys Arg Ile Ser Ile Ser Lys Gln Leu Ala Ser Val Lys Ala	
30 35 40 45	
ctg agg aag tgc tca gat ctg gaa aaa gct att gcc acc act gct ctg	194
Leu Arg Lys Cys Ser Asp Leu Glu Lys Ala Ile Ala Thr Thr Ala Leu	
46 51 56 61	
att ttc aga aat tct tct gac tct gat ggt aaa ctt gaa aaa gct att	242
Ile Phe Arg Asn Ser Ser Asp Ser Asp Gly Lys Leu Glu Lys Ala Ile	
62 67 72 77	
gcc aaa gat ctg ctg caa acc caa ttt agg aat ttc gca gag gga caa	290
Ala Lys Asp Leu Leu Gln Thr Gln Phe Arg Asn Phe Ala Glu Gly Gln	
78 83 88 93	
gaa acc aag cca aaa tac aga gag atc ctt tct gaa ctt gat gag cac	338
Glu Thr Lys Pro Lys Tyr Arg Glu Ile Leu Ser Glu Leu Asp Glu His	
94 99 104 109	
aca gaa aat aag cta gat ttt gaa gac ttc atg atc ttg ctc tta agc	386
Thr Glu Asn Lys Leu Asp Phe Glu Asp Phe Met Ile Leu Leu Ser	
110 115 120 125	
atc act gtc atg tca gat ctg cta caa aat ata cgg aat gta aaa att	434
Ile Thr Val Met Ser Asp Leu Leu Gln Asn Ile Arg Asn Val Lys Ile	
126 131 136 141	
atg aaa tga acagttc taaatatgct gtataaaaata atggcaaaag acagtgttat	490
Met Lys *	
142	
taaaatgttt ccatcttatt tgtgattaat tgaatatatc tatcaacgaa atcgctgaca	550
gcgaaagtcga cccggaaatt ccgaaca	577

<210> 1076

<211> 6481

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (335)..(6481)

<400> 1076

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gtttagctt	gtcatgtttt	gaacagctgt	ctatggaaag	aaagcaaaca	caacctagag	120
caacattgat	ttgttttaga	aagctctttt	atttcagtt	ctggctgtgt	tcaacatctt	180
agcttacgtt	tttcatgttg	taatgatctg	ccgtacggac	gatcacctct	aagtttagaga	240
gttctgtaat	ttggcttgg	ttaaagatgc	ttggtagtg	aaagctgctg	cttttttat	300
agtcaaagga	ctggttctga	gaggcttgtt	gcag	atg gct gag gtc acc gtc	Met Ala Glu Val Thr Val	352
					1	
cca agg gtg tat gtc	gtg ttt ggc atc cat	tgc atc atg	gct gtc aag gca			400
Pro Arg Val Tyr Val Val Phe	Gly Ile His Cys Ile Met Ala Lys Ala					
7	12	17	22			
tct tca gat gtg cag gtt	tca ggc ttt cat	cggtt	aaa atc cag cac	gtt		448
Ser Ser Asp Val Gln Val Ser Gly Phe His Arg Lys Ile Gln His Val						
23	28	33	38			
aaa aat gaa ctt tgc cac atg ttg agc ttg gag gag	gtg gcc cca gtg					496
Lys Asn Glu Leu Cys His Met Leu Ser Leu Glu Glu Val Ala Pro Val						
39	44	49	54			
ctg cag cag aca tta ctt cag gac aac ctc ttg ggc	agg gta cat ttt					544
Leu Gln Gln Thr Leu Leu Gln Asp Asn Leu Leu Gly Arg Val His Phe						
55	60	65	70			
gac caa ttt aaa gaa gca tta ata ctc atc ttg tcc	aga act ctg tca					592
Asp Gln Phe Lys Glu Ala Leu Ile Leu Ile Leu Ser Arg Thr Leu Ser						
71	76	81	86			
gat gaa gaa cac ttc caa gaa cca gac tgc tca cta	gaa gct cag ccc					640
Asp Glu Glu His Phe Gln Glu Pro Asp Cys Ser Leu Glu Ala Gln Pro						
87	92	97	102			
aga tat gtt aga ggt gag aag cct tac gga cga	agg tcc ttg ccc gag					688
Arg Tyr Val Arg Gly Glu Lys Pro Tyr Gly Arg Arg Ser Leu Pro Glu						
103	108	113	118			
ttc caa gag tcc gtg gag gag ttt cct gag gtg acg	gtg att gag ccc					736
Phe Gln Glu Ser Val Glu Glu Phe Pro Glu Val Thr Val Ile Glu Pro						
119	124	129	134			

ctg gat gaa gaa gcg cgg cct tca cac atc cca gcc ggt gac tgc agt		784	
Leu Asp Glu Glu Ala Arg Pro Ser His Ile Pro Ala Gly Asp Cys Ser			
135	140	145	150
gag cac tgg aag acg caa cgc agt gag gag tat gaa gcg gaa ggc cag		832	
Glu His Trp Lys Thr Gln Arg Ser Glu Glu Tyr Glu Ala Glu Gly Gln			
151	156	161	166
tta agg ttt tgg aac cca gat gac ttg aat gct tca cag agt gga tct		880	
Leu Arg Phe Trp Asn Pro Asp Asp Leu Asn Ala Ser Gln Ser Gly Ser			
167	172	177	182
tcc cct ccc caa gac tgg ata gaa gag aaa ctg caa caa gtt tgt gaa		928	
Ser Pro Pro Gln Asp Trp Ile Glu Glu Lys Leu Gln Gln Val Cys Glu			
183	188	193	198
gat ttg ggg atc acc cct gat ggt cac ctg aac cg ^g aag aag ctg gtt		976	
Asp Leu Gly Ile Thr Pro Asp Gly His Leu Asn Arg Lys Lys Leu Val			
199	204	209	214
tcc atc tgt gag cag tat ggt ttg cag aat gtg gat gga gag atg ctc		1024	
Ser Ile Cys Glu Gln Tyr Gly Leu Gln Asn Val Asp Gly Glu Met Leu			
215	220	225	230
gag gaa gta ttc cat aat ctt gat cct gac ggt aca atg agt gta gaa		1072	
Glu Glu Val Phe His Asn Leu Asp Pro Asp Gly Thr Met Ser Val Glu			
231	236	241	246
gat ttt ttc tat ggt ttg ttt aaa aat gga aaa tct ctt aca cca tca		1120	
Asp Phe Phe Tyr Gly Leu Phe Lys Asn Gly Lys Ser Leu Thr Pro Ser			
247	252	257	262
gca tct act cca tat aga caa cta aaa agg cac ctt tcc atg cag tct		1168	
Ala Ser Thr Pro Tyr Arg Gln Leu Lys Arg His Leu Ser Met Gln Ser			
263	268	273	278
tcc gat gag agt gga cga cgt acc aca acc tca tca gca acg aca agt		1216	
Phe Asp Glu Ser Gly Arg Arg Thr Thr Ser Ser Ala Thr Thr Ser			
279	284	289	294
acc att ggc ttt cgg gtc ttc tcc tgc ctg gat gat ggg atg ggc cat		1264	
Thr Ile Gly Phe Arg Val Phe Ser Cys Leu Asp Asp Gly Met Gly His			
295	300	305	310
gca tct gtg gag agg ata ctc gac acc tgg cag gaa gag ggc att gag		1312	
Ala Ser Val Glu Arg Ile Leu Asp Thr Trp Gln Glu Glu Gly Ile Glu			
311	316	321	326
aac agc cag gag atc ctg aag gcc ttg gat ttc agc ctc gat gga aac		1360	
Asn Ser Gln Glu Ile Leu Lys Ala Leu Asp Phe Ser Leu Asp Gly Asn			
327	332	337	342
atc aat ttg aca gaa tta aca ctg gcc ctt gaa aat gaa ctt ttg gtt		1408	
Ile Asn Leu Thr Glu Leu Thr Leu Ala Leu Glu Asn Glu Leu Leu Val			
343	348	353	358

acc aag aac agc att cac cag gcg gct ctg gcc agc ttt aag gct gaa			1456
Thr Lys Asn Ser Ile His Gln Ala Ala Leu Ala Ser Phe Lys Ala Glu			
359	364	369	374
atc cgg cat ttg ttg gaa cga gtt gat cag gtg gtc aga gaa aaa gag			1504
Ile Arg His Leu Leu Glu Arg Val Asp Gln Val Val Arg Glu Lys Glu			
375	380	385	390
aag cta cgg tca gat ctg gac aag gcc gag aag ctc aag tct tta atg			1552
Lys Leu Arg Ser Asp Leu Asp Lys Ala Glu Lys Leu Lys Ser Leu Met			
391	396	401	406
gcc tcg gag gtg gat gat cac cat gcg gcc ata gag cgg cgg aat gag			1600
Ala Ser Glu Val Asp Asp His His Ala Ala Ile Glu Arg Arg Asn Glu			
407	412	417	422
tac aac ctc agg aaa ctg gat gaa gag tac aag gag cga ata gca gcc			1648
Tyr Asn Leu Arg Lys Leu Asp Glu Glu Tyr Lys Glu Arg Ile Ala Ala			
423	428	433	438
tta aaa aat gaa ctc cga aaa gag aga gag cag atc ctg cag cag gca			1696
Leu Lys Asn Glu Leu Arg Lys Glu Arg Glu Gln Ile Leu Gln Gln Ala			
439	444	449	454
ggc aag cag cgt tta gaa ctt gaa cag gaa att gaa aag gca aaa aca			1744
Gly Lys Gln Arg Leu Glu Leu Glu Gln Glu Ile Glu Lys Ala Lys Thr			
455	460	465	470
gaa gag aac tat atc cgg gac cgc ctt gcc ctc tct tta aag gaa aac			1792
Glu Glu Asn Tyr Ile Arg Asp Arg Leu Ala Leu Ser Leu Lys Glu Asn			
471	476	481	486
agt cgt ctg gaa aat gag ctt cta gaa aat gca gag aag ttg gca gaa			1840
Ser Arg Leu Glu Asn Glu Leu Leu Glu Asn Ala Glu Lys Leu Ala Glu			
487	492	497	502
tat gag aat ctg aca aac aaa ctt cag aga aat ttg gaa aat gtg tta			1888
Tyr Glu Asn Leu Thr Asn Lys Leu Gln Arg Asn Leu Glu Asn Val Leu			
503	508	513	518
gca gaa aag ttt ggt gac ctc gat cct agc agt gct gag ttc ttc ctg			1936
Ala Glu Lys Phe Gly Asp Leu Asp Pro Ser Ser Ala Glu Phe Phe Leu			
519	524	529	534
caa gaa gag aga ctg aca cag atg aga aat gaa tat gag cgg cag tgc			1984
Gln Glu Arg Leu Thr Gln Met Arg Asn Glu Tyr Glu Arg Gln Cys			
535	540	545	550
agg gta cta caa gac caa gta gat gaa ctc cag tct gag ctg gaa gaa			2032
Arg Val Leu Gln Asp Gln Val Asp Glu Leu Gln Ser Glu Leu Glu Glu			
551	556	561	566
tat cgt gca caa ggc aga gtg ctc agg ctt ccg ttg aag aac tca ccg			2080
Tyr Arg Ala Gln Gly Arg Val Leu Arg Leu Pro Leu Lys Asn Ser Pro			
567	572	577	582
tca gaa gaa gtt gag gct aac agc ggt ggc att gaa ccc gaa cac ggg			2128

Ser	Glu	Glu	Val	Glu	Ala	Asn	Ser	Gly	Gly	Ile	Glu	Pro	Glu	His	Gly		
583				588				593			598						
ctc	ggt	tct	gaa	gaa	tgc	aat	cca	ttg	aat	atg	agc	att	gag	gca	gag	2176	
Leu	Gly	Ser	Glu	Glu	Cys	Asn	Pro	Leu	Asn	Met	Ser	Ile	Glu	Ala	Glu		
599					604				609			614					
ctg	gtc	att	gaa	cag	atg	aaa	gaa	caa	cat	cac	agg	gac	ata	tgt	tgc	2224	
Leu	Val	Ile	Glu	Gln	Met	Lys	Glu	Gln	His	His	Arg	Asp	Ile	Cys	Cys		
615					620				625			630					
ctc	aga	ctg	gag	ctc	gaa	gat	aaa	gtg	cgc	cat	tat	gaa	aag	cag	ctg	2272	
Leu	Arg	Leu	Glu	Leu	Glu	Asp	Lys	Val	Arg	His	Tyr	Glu	Lys	Gln	Leu		
631					636				641			646					
gac	gaa	acc	gtg	gtc	agc	tgc	aag	aag	gca	cag	gag	aac	atg	aag	caa	2320	
Asp	Glu	Thr	Val	Val	Ser	Cys	Lys	Lys	Ala	Gln	Glu	Asn	Met	Lys	Gln		
647					652				657			662					
agg	cat	gag	aac	gaa	acg	cac	acc	tta	gaa	aaa	caa	ata	agt	gac	ctt	2368	
Arg	His	Glu	Asn	Glu	Thr	His	Thr	Leu	Glu	Lys	Gln	Ile	Ser	Asp	Leu		
663					668				673			678					
aaa	atg	aaa	att	gct	gaa	ctt	cag	ggg	caa	gca	gca	gtg	ctc	aag	gag	2416	
Lys	Met	Lys	Ile	Ala	Glu	Leu	Gln	Gly	Gln	Ala	Ala	Val	Leu	Lys	Glu		
679					684				689			694					
gca	cat	cat	gag	gcc	act	tgc	agg	cat	gag	gag	gag	aaa	aaa	caa	ctg	2464	
Ala	His	His	Glu	Ala	Thr	Cys	Arg	His	Glu	Glu	Glu	Lys	Lys	Gln	Leu		
695					700				705			710					
caa	gtg	aag	ctt	gag	gag	gaa	aag	act	cac	ctg	cag	gag	aag	ctg	agg	2512	
Gln	Val	Lys	Leu	Glu	Glu	Lys	Thr	His	Leu	Gln	Glu	Lys	Leu	Arg			
711					716				721			726					
ctg	caa	cat	gag	atg	gag	ctc	aag	gct	aga	ctg	aca	cag	gct	caa	gca	2560	
Leu	Gln	His	Glu	Met	Glu	Leu	Lys	Ala	Arg	Leu	Thr	Gln	Ala	Gln	Ala		
727					732				737			742					
agc	ttt	gag	cgg	gag	agg	gaa	ggc	ctt	cag	agt	agc	gcc	tgg	aca	gaa	2608	
Ser	Phe	Glu	Arg	Glu	Arg	Gly	Leu	Gln	Ser	Ser	Ala	Trp	Thr	Glu			
743					748				753			758					
gag	aag	gtg	aga	ggc	ttg	act	cag	gaa	cta	gag	cag	ttt	cac	cag	gag	2656	
Glu	Lys	Val	Arg	Gly	Leu	Thr	Gln	Glu	Leu	Glu	Gln	Phe	His	Gln	Glu		
759					764				769			774					
cag	ctg	aca	agc	ctg	gtg	gag	aaa	cac	act	ctt	gag	aaa	gag	gag	tta	2704	
Gln	Leu	Thr	Ser	Leu	Val	Glu	Lys	His	Thr	Leu	Glu	Lys	Glu	Glu	Leu		
775					780				785			790					
aga	aaa	gag	ctc	ttg	gaa	aag	cac	caa	agg	gag	ctt	cag	gag	gga	agg	2752	
Arg	Lys	Glu	Leu	Leu	Glu	Lys	His	Gln	Arg	Glu	Leu	Gln	Glu	Gly	Arg		
791					796				801			806					
gaa	aaa	atg	gaa	aca	gag	tgt	aat	aga	aga	acc	tct	caa	ata	gaa	gcc	2800	
Glu	Lys	Met	Glu	Thr	Glu	Cys	Asn	Arg	Arg	Arg	Thr	Ser	Gln	Ile	Glu	Ala	

807	812	817	822	
cag ttt cag tct gat tgt cag aaa gtc act gag agg tgt gaa agc gct Gln Phe Gln Ser Asp Cys Gln Lys Val Thr Glu Arg Cys Glu Ser Ala 823	828	833	838	2848
ctg caa agc ctg gag ggg cgc tac cgc caa gag ctg aag gac ctc cag Leu Gln Ser Leu Glu Gly Arg Tyr Arg Gln Glu Leu Lys Asp Leu Gln 839	844	849	854	2896
gaa cag cag cgt gag gag aaa tcc cag tgg gaa ttt gag aag gac gag Glu Gln Gln Arg Glu Glu Lys Ser Gln Trp Glu Phe Glu Lys Asp Glu 855	860	865	870	2944
ctc acc cag gag tgt gcg gaa gca cag gag ctg ctg aaa gag act ctt Leu Thr Gln Glu Cys Ala Glu Ala Gln Glu Leu Leu Lys Glu Thr Leu 871	876	881	886	2992
aag aga gag aaa aca act tct ctg gtc ctg acc cag gag aga gag atg Lys Arg Glu Lys Thr Thr Ser Leu Val Leu Thr Gln Glu Arg Glu Met 887	892	897	902	3040
ctg gag aaa aca tac aaa gac cat ttg aac agc atg gtc gtc gag aga Leu Glu Lys Thr Tyr Lys Asp His Leu Asn Ser Met Val Val Glu Arg 903	908	913	918	3088
cag cag cta ctccaa gac ctg gaa gac cta aga aat gta tct gaa acc Gln Gln Leu Leu Gln Asp Leu Glu Asp Leu Arg Asn Val Ser Glu Thr 919	924	929	934	3136
cag caa agc ctg ctg tct gac cag ata ctt gag ctg aag agc agt cac Gln Gln Ser Leu Leu Ser Asp Gln Ile Leu Glu Leu Lys Ser Ser His 935	940	945	950	3184
aaa agg gaa ctg agg gag cgt gag gag gtc ctg tgc cag cag ggg gtc Lys Arg Glu Leu Arg Glu Glu Glu Val Leu Cys Gln Gln Gly Val 951	956	961	966	3232
tcg gag cag ctg gcc agc cag cgg ctg gaa aga cta gaa atg gaa cat Ser Glu Gln Leu Ala Ser Gln Arg Leu Glu Arg Leu Glu Met Glu His 967	972	977	982	3280
gac cag gaa agg cag gaa atg atg tcc aag ctt cta gcc atg gag aac Asp Gln Glu Arg Gln Glu Met Met Ser Lys Leu Leu Ala Met Glu Asn 983	988	993	998	3328
att cac aaa gcg acc tgt gag aca gca gat cga gaa aga gcc gag atg Ile His Lys Ala Thr Cys Glu Thr Ala Asp Arg Glu Arg Ala Glu Met 999	1004	1009	1014	3376
agc aca gaa atc tcc aga ctt cag agt aaa ata aag gaa atg cag cag Ser Thr Glu Ile Ser Arg Leu Gln Ser Lys Ile Lys Glu Met Gln Gln 1015	1020	1025	1030	3424
gca aca tct cct ctc tct atg ctt cag agt ggt tgc cag gtg ata gga Ala Thr Ser Pro Leu Ser Met Leu Gln Ser Gly Cys Gln Val Ile Gly 1031	1036	1041	1046	3472

gag gag gag gtg gaa gga gat gga gcc ctg tcc ctg ctt cag aaa ggg Glu Glu Glu Val Glu Gly Asp Gly Ala Leu Ser Leu Leu Gln Lys Gly	3520
1047 1052 1057 1062	
 gag cag ctg ttg gaa gaa aat ggg gac gtc ctc tta agc ctg cag aga Glu Gln Leu Leu Glu Glu Asn Gly Asp Val Leu Leu Ser Leu Gln Arg	3568
1063 1068 1073 1078	
 gct cat gaa cag gca gtg aag gaa aat gtg aaa atg gct act gaa att Ala His Glu Gln Ala Val Lys Glu Asn Val Lys Met Ala Thr Glu Ile	3616
1079 1084 1089 1094	
 tct aga ttg caa cag agg cta caa aag tta gag cca ggg tta gta atg Ser Arg Leu Gln Arg Leu Gln Lys Leu Glu Pro Gly Leu Val Met	3664
1095 1100 1105 1110	
 tct tct tgt ttg gat gag cca gct act gag ttt ttt gga aat act gcg Ser Ser Cys Leu Asp Glu Pro Ala Thr Glu Phe Phe Gly Asn Thr Ala	3712
1111 1116 1121 1126	
 gaa caa aca gag ccg ttt tta cag caa aac cga acg aag caa gta gaa Glu Gln Thr Glu Pro Phe Leu Gln Gln Asn Arg Thr Lys Gln Val Glu	3760
1127 1132 1137 1142	
 ggg gtg acc agg cgg cat gtc cta agt gac ctg gaa gat gat gag gtc Gly Val Thr Arg Arg His Val Leu Ser Asp Leu Glu Asp Asp Glu Val	3808
1143 1148 1153 1158	
 cg ^g gac ctg gga agt aca ggg acg agc tct gtt cag aga cag gaa gtc Arg Asp Leu Gly Ser Thr Gly Thr Ser Ser Val Gln Arg Gln Glu Val	3856
1159 1164 1169 1174	
 aaa ata gag gag tct gaa gct tca gta gag ggt ttt tcc gag ctt gaa Lys Ile Glu Glu Ser Glu Ala Ser Val Glu Gly Phe Ser Glu Leu Glu	3904
1175 1180 1185 1190	
 aac agt gaa gag acc agg act gaa tcc tgg gag ctg aaa aat cac att Asn Ser Glu Glu Thr Arg Thr Glu Ser Trp Glu Leu Lys Asn His Ile	3952
1191 1196 1201 1206	
 agt ctg ctt cag gaa cag ctc atg atg ttt tgt gcg gac tgt gat cta Ser Leu Leu Gln Glu Gln Leu Met Met Phe Cys Ala Asp Cys Asp Leu	4000
1207 1212 1217 1222	
 gct tct gaa aag aaa cag gag cta ctt ttt gat gtt tct gtg ctc aaa Ala Ser Glu Lys Lys Gln Glu Leu Leu Phe Asp Val Ser Val Leu Lys	4048
1223 1228 1233 1238	
 aag aaa ctg aaa atc ctt gag aga atc cct gag gct tct ccc aga tat Lys Lys Leu Lys Ile Leu Glu Arg Ile Pro Glu Ala Ser Pro Arg Tyr	4096
1239 1244 1249 1254	
 aag ctg ttg tat gaa gat gtg agc cga gaa aat gac tgc ctt cag gaa Lys Leu Leu Tyr Glu Asp Val Ser Arg Glu Asn Asp Cys Leu Gln Glu	4144
1255 1260 1265 1270	

gag ctg gag atg gag aca cgc tac gat gag gca cta gaa aat aac Glu Leu Glu Met Met Glu Thr Arg Tyr Asp Glu Ala Leu Glu Asn Asn	4192
1271 1276 1281 1286	
aaa gaa ctc act gca gag gtt ttc agg ttg cag gat gag ctg aag aaa Lys Glu Leu Thr Ala Glu Val Phe Arg Leu Gln Asp Glu Leu Lys Lys	4240
1287 1292 1297 1302	
atg gag gaa gtc act gaa aca ttc ctc agc ctg gaa aag agt tac gat Met Glu Glu Val Thr Glu Thr Phe Leu Ser Leu Glu Lys Ser Tyr Asp	4288
1303 1308 1313 1318	
gag gtc aaa ata gaa aat gag gag ctg aat gtt ctg gtt ttg aga ctt Glu Val Lys Ile Glu Asn Glu Glu Leu Asn Val Leu Val Leu Arg Leu	4336
1319 1324 1329 1334	
caa ggc aag att gag aag ctt cac gag agc gtg gtc aag cgg tgt gac Gln Gly Lys Ile Glu Lys Leu His Glu Ser Val Val Lys Arg Cys Asp	4384
1335 1340 1345 1350	
tgc tgc tta tgg gaa ggc agt tta gag aac ctg gaa atc gaa cct gat Cys Cys Leu Trp Glu Gly Ser Leu Glu Asn Leu Glu Ile Glu Pro Asp	4432
1351 1356 1361 1366	
gga aat ata ctc cag ctc aat cag aca ctg gaa gag tgt gtg ccc agg Gly Asn Ile Leu Gln Leu Asn Gln Thr Leu Glu Glu Cys Val Pro Arg	4480
1367 1372 1377 1382	
gtt agg agt gta cat cat gtc ata gag gaa tgt aag caa gaa aac cag Val Arg Ser Val His His Val Ile Glu Glu Cys Lys Gln Glu Asn Gln	4528
1383 1388 1393 1398	
tac ctt gag ggg aac aca cag ctc ttg gaa aaa gta aaa gca cat gaa Tyr Leu Glu Gly Asn Thr Gln Leu Leu Glu Lys Val Lys Ala His Glu	4576
1399 1404 1409 1414	
att gcc tgg ttt cat gga aca att cag aca cat cac gaa cgg cct aga Ile Ala Trp Phe His Gly Thr Ile Gln Thr His His Glu Arg Pro Arg	4624
1415 1420 1425 1430	
gta cag aat caa ttt ata ctg gag gaa aac act act ctc cta ggc ttt Val Gln Asn Gln Phe Ile Leu Glu Glu Asn Thr Thr Leu Leu Gly Phe	4672
1431 1436 1441 1446	
caa aac aaa cat ttt cag cat cag gcc aca ttg cca aat tta gaa ctg Gln Asn Lys His Phe Gln His Gln Ala Thr Leu Pro Asn Leu Glu Leu	4720
1447 1452 1457 1462	
gaa aaa caa aat ttc cag gag ctg act agg aat ttg agg gaa aaa ttc Glu Lys Gln Asn Phe Gln Glu Leu Thr Arg Asn Leu Arg Glu Lys Phe	4768
1463 1468 1473 1478	
cct att tta att tac caa aaa aat ttt ctt tct ccc gga aaa aag gag Pro Ile Leu, Ile Tyr Gln Lys Asn Phe Leu Ser Pro Gly Lys Lys Glu	4816
1479 1484 1489 1494	
gaa gaa ctg aag gca atg atg cat gac ttg caa atc cct tgc agt gaa	4864

Glu	Glu	Leu	Lys	Ala	Met	Met	His	Asp	Leu	Gln	Ile	Pro	Cys	Ser	Glu	
1495																1510
atg	cag	caa	aag	gtt	gaa	ctt	ctg	aaa	tat	gaa	tct	gaa	aag	ctt	cac	4912
Met	Gln	Gln	Lys	Val	Glu	Leu	Leu	Lys	Tyr	Glu	Ser	Glu	Lys	Leu	His	
1511																1526
cag	gaa	aat	tct	ttt	ttg	aga	aat	gaa	att	act	act	tta	aat	gaa	gaa	4960
Gln	Glu	Asn	Ser	Phe	Leu	Arg	Asn	Glu	Ile	Thr	Thr	Leu	Asn	Glu	Glu	
1527																1542
gat	agc	att	tct	aac	ctg	aaa	tta	ggg	aca	tta	aat	gga	tct	cag	gaa	5008
Asp	Ser	Ile	Ser	Asn	Leu	Lys	Leu	Gly	Thr	Leu	Asn	Gly	Ser	Gln	Glu	
1543																1558
gaa	atg	tgg	caa	aaa	acg	gaa	tct	gta	aaa	caa	gaa	aat	gct	gca	gtt	5056
Glu	Met	Trp	Gln	Lys	Thr	Glu	Ser	Val	Lys	Gln	Glu	Asn	Ala	Ala	Val	
1559																1574
ctg	aag	atg	gtt	gaa	aat	tta	aag	aaa	cag	att	tca	gaa	tta	aaa	atc	5104
Leu	Lys	Met	Val	Glu	Asn	Leu	Lys	Lys	Gln	Ile	Ser	Glu	Leu	Lys	Ile	
1575																1590
aaa	aac	caa	caa	ttg	gat	ttg	gaa	aat	aca	gaa	ctt	agc	caa	aag	aac	5152
Lys	Asn	Gln	Gln	Leu	Asp	Leu	Glu	Asn	Thr	Glu	Leu	Ser	Gln	Lys	Asn	
1591																1606
tct	cca	aac	cag	gaa	aaa	ctg	caa	gaa	ctt	aat	caa	ctg	cta	aca	gaa	5200
Ser	Pro	Asn	Gln	Glu	Lys	Leu	Gln	Glu	Leu	Asn	Gln	Leu	Leu	Thr	Glu	
1607																1622
atg	cta	tgc	cag	aag	gaa	aaa	gag	cca	gga	aac	agt	gca	ttg	gag	gaa	5248
Met	Leu	Cys	Gln	Lys	Glu	Lys	Glu	Pro	Gly	Asn	Ser	Ala	Leu	Glu	Glu	
1623																1638
cgg	gaa	caa	gag	aag	ttt	aat	ctg	aaa	gaa	gaa	ccg	gaa	cgt	tgt	aaa	5296
Arg	Glu	Gln	Glu	Lys	Phe	Asn	Leu	Lys	Glu	Glu	Pro	Glu	Arg	Cys	Lys	
1639																1654
gtg	cag	tcc	tcc	act	tta	gtg	tct	tct	ctg	gag	gcf	gag	ctc	tct	gaa	5344
Val	Gln	Ser	Ser	Thr	Leu	Val	Ser	Ser	Leu	Glu	Ala	Glu	Leu	Ser	Glu	
1655																1670
gtt	aac	tac	agg	acc	cct	att	gtg	caa	cag	gaa	aac	ccc	ctt	ctc	caa	5392
Val	Asn	Tyr	Arg	Thr	Pro	Ile	Val	Gln	Gln	Glu	Asn	Pro	Leu	Leu	Gln	
1671																1686
gat	gaa	ctg	gag	aaa	atg	aaa	cag	ctg	cac	aga	tgt	ccc	gat	ctc	tcg	5440
Asp	Glu	Leu	Glu	Lys	Met	Lys	Gln	Leu	His	Arg	Cys	Pro	Asp	Leu	Ser	
1687																1702
aac	ttc	cag	caa	aaa	atc	tct	agt	gtt	cta	agc	tac	aac	gaa	aaa	ctg	5488
Asn	Phe	Gln	Gln	Lys	Ile	Ser	Ser	Val	Leu	Ser	Tyr	Asn	Glu	Lys	Leu	
1703																1718
ctg	aaa	gaa	aag	gaa	gct	agt	gag	gaa	tta	aat	agc	tgt	gtc	gat		5536
Leu	Lys	Glu	Lys	Glu	Ala	Leu	Ser	Glu	Glu	Leu	Asn	Ser	Cys	Val	Asp	

1719	1724	1729	1734	
aag ttg gca aaa tca agt ctt tta gag cat aga att gcg acg atg aag Lys Leu Ala Lys Ser Ser Leu Leu Glu His Arg Ile Ala Thr Met Lys				5584
1735 1740 1745 1750				
cag gaa cag aaa tcc tgg gaa cat cag agt gcg agc tta aag aca cag Gln Glu Gln Lys Ser Trp Glu His Gln Ser Ala Ser Leu Lys Thr Gln				5632
1751 1756 1761 1766				
ctg gtg gct tct cag gaa aag gtt cag aat tta gaa gac acc gtg cag Leu Val Ala Ser Gln Glu Lys Val Gln Asn Leu Glu Asp Thr Val Gln				5680
1767 1772 1777 1782				
aat gta aac ctg caa atg tcc cgg atg aaa tct gac cca cga gtg act Asn Val Asn Leu Gln Met Ser Arg Met Lys Ser Asp Pro Arg Val Thr				5728
1783 1788 1793 1798				
cag cag gaa aag gag gct tta aaa caa gaa gtg atg cct tta cat aag Gln Gln Glu Lys Glu Ala Leu Lys Gln Glu Val Met Pro Leu His Lys				5776
1799 1804 1809 1814				
caa ctt cag aat tct gtg gca aga gct ggc ccc aga gag ata gat cat Gln Leu Gln Asn Ser Val Ala Arg Ala Gly Pro Arg Glu Ile Asp His				5824
1815 1820 1825 1830				
cca tca ggg ttc cat aac cag cag aaa agg ctg tct tgg gac aag ttg Pro Ser Gly Phe His Asn Gln Gln Lys Arg Leu Ser Trp Asp Lys Leu				5872
1831 1836 1841 1846				
gat tat ctg atg aat gag gaa cag cag ttg ttt tgc aaa gag aat gag Asp Tyr Leu Met Asn Glu Glu Gln Leu Phe Cys Lys Glu Asn Glu				5920
1847 1852 1857 1862				
agg ttc cag acc atg gta cag aac acc aaa gcc gaa tta acg cat tcc Arg Phe Gln Thr Met Val Gln Asn Thr Lys Ala Glu Leu Thr His Ser				5968
1863 1868 1873 1878				
cgg gag aag ttc cgt cag ttg gaa tcc aat ctt ctt ccc aag cac caa Arg Glu Lys Phe Arg Gln Leu Glu Ser Asn Leu Leu Pro Lys His Gln				6016
1879 1884 1889 1894				
aaa tat tta aac cca tca ggt acc atg aat ccc aca gag caa gaa aaa Lys Tyr Leu Asn Pro Ser Gly Thr Met Asn Pro Thr Glu Gln Glu Lys				6064
1895 1900 1905 1910				
ttg agc tta aag aga gag tgt gat cag ttt cag aaa gaa caa tct cct Leu Ser Leu Lys Arg Glu Cys Asp Gln Phe Gln Lys Glu Gln Ser Pro				6112
1911 1916 1921 1926				
gct aac agg aag gtc agt cag atg aat tcc ctt gaa caa gaa tta aaa Ala Asn Arg Lys Val Ser Gln Met Asn Ser Leu Glu Gln Glu Leu Lys				6160
1927 1932 1937 1942				
aca att cat ttg gaa aat gaa ggc ctg aaa aag aaa caa gta aaa ctg Thr Ile His Leu Glu Asn Glu Gly Leu Lys Lys Gln Val Lys Leu				6208
1943 1948 1953 1958				

gat gag cag ctc atg gag atg cag cac ctg agg tcc act gcg acg cct		6256	
Asp Glu Gln Leu Met Glu Met Gln His Leu Arg Ser Thr Ala Thr Pro			
1959	1964	1969	1974
agc ccg tcc cct cat gct tgg gat ttg cag ctg ctc cag cag caa gcg		6304	
Ser Pro Ser Pro His Ala Trp Asp Leu Gln Leu Gln Gln Gln Ala			
1975	1980	1985	1990
tgc cgg atg gtg ccc agg gag cag ttt ttg cgg ttt aaa ccc cag ttg		6352	
Cys Arg Met Val Pro Arg Glu Gln Phe Leu Arg Phe Lys Pro Gln Leu			
1991	1996	2001	2006
ctg cag gca gaa agg ata agc cag cac ttg cag ggg gaa ttt gaa aac		6400	
Leu Gln Ala Glu Arg Ile Ser Gln His Leu Gln Gly Glu Phe Glu Asn			
2007	2012	2017	2022
agg acc tcc gaa acc aac aca cca cgg gga aac cgg gaa caa ttg gta		6448	
Arg Thr Ser Glu Thr Asn Thr Pro Arg Gly Asn Arg Glu Gln Leu Val			
2023	2028	2033	2038
act gtc atg ggg gga acg aat gat aga agt tga		6481	
Thr Val Met Gly Gly Thr Asn Asp Arg Ser *			
2039	2044	2049	
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accgggtccgg aattcccgaa tcgacccacg cgtccgcgag aggcacagcg	atg ggc	116	
	Met Gly		
	1		
tcc gtg ctg agc acc gac agc ggc aaa tcg gcg ccc gcc tct gcc acc		164	
Ser Val Leu Ser Thr Asp Ser Gly Lys Ser Ala Pro Ala Ser Ala Thr			
3	8	13	18
gcg cgg gcc ctg gag cgc agg gac ccg gag ttg ccc gtc acg tcc		212	
Ala Arg Ala Leu Glu Arg Arg Asp Pro Glu Leu Pro Val Thr Ser			
19	24	29	34

ttc gac tgc gcc gtg tgc ctt gag gtg tta cac cag cct gtc cg ^g acc Phe Asp Cys Ala Val Cys Leu Glu Val Leu His Gln Pro Val Arg Thr 35 40 45 50	260
cgc tgt ggc cac gta ttc tgc cgt tcc tgt att gct acc agt cta aag Arg Cys Gly His Val Phe Cys Arg Ser Cys Ile Ala Thr Ser Leu Lys 51 56 61 66	308
aac aac aag tgg acc tgt cct tat tgc cg ^g gca tat ctt cct tca gaa Asn Asn Lys Trp Thr Cys Pro Tyr Cys Arg Ala Tyr Leu Pro Ser Glu 67 72 77 82	356
gga gtt cca gca act gat gta gcc aaa aga atg aaa tca gag tat aag Gly Val Pro Ala Thr Asp Val Ala Lys Arg Met Lys Ser Glu Tyr Lys 83 88 93 98	404
aac tgc gct gag tgt gac acc ctg gtt tgc ctc agt gaa atg agg gca Asn Cys Ala Glu Cys Asp Thr Leu Val Cys Leu Ser Glu Met Arg Ala 99 104 109 114	452
cat att cgg act tgt cag aag tac ata gat aag tat gga cca cta caa His Ile Arg Thr Cys Gln Lys Tyr Ile Asp Lys Tyr Gly Pro Leu Gln 115 120 125 130	500
gaa ctt gag gag aca gca gca agg tgt gta tgt ccc ttt tgt cag agg Glu Leu Glu Glu Thr Ala Ala Arg Cys Val Cys Pro Phe Cys Gln Arg 131 136 141 146	548
gaa ctg tat gaa gac agc ttg ctg gat cat tgt att act cat cac aga Glu Leu Tyr Glu Asp Ser Leu Leu Asp His Cys Ile Thr His His Arg 147 152 157 162	596
tcg gaa cg ^g agg cct gtg ttc tgt cca ctt tgc cgt tta ata ccc gat Ser Glu Arg Arg Pro Val Phe Cys Pro Leu Cys Arg Leu Ile Pro Asp 163 168 173 178	644
gag aat cca agc agc ttc agt ggc agt tta ata aga cat ctg caa gtt Glu Asn Pro Ser Ser Phe Ser Gly Ser Leu Ile Arg His Leu Gln Val 179 184 189 194	692
agt cac act ttg ttt tat gat gat ttc ata gat ttt aat ata att gag Ser His Thr Leu Phe Tyr Asp Asp Phe Ile Asp Phe Asn Ile Ile Glu 195 200 205 210	740
gaa gct ctt atc cga aga gtc tta gac cg ^g tca ctt ctt gaa tat gtg Glu Ala Leu Ile Arg Arg Val Leu Asp Arg Ser Leu Leu Glu Tyr Val 211 216 221 226	788
aat cac tcg aac acc aca taa tt ttat ^{aaaa} ac gaagg ^{aaaa} gggaccactg Asn His Ser Asn Thr Thr *	841
227 232	
aattgcacca tttaagatgc tgcttgaaca aatggggagg aagttgtcaa tgattgtatgg	901
gcaaaaatgt acaacacagt tatgtgtttg tccatgttta ttgttatagt gcattaaaa	961

actgctttaa ttttaatggt taaaatctgt tttacatcct tgagattctt acacatctaa	1021
caacaaaaaa aattatctac atcagtcatt gttacatgga aaagacaggt ggtaggcaag	1081
taggtggagg atctcggtt gcaaattaga taatactctg tgtataatgc tacatatccg	1141
gacgcgtggg tcgaccggg aattccggac cggtacctgc aggcgtacca gcttcccta	1201
tagtgagtgc tttnancctc ggcgtcacac tcgta	1236

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gggggctccg aggccggggtc tgggtgttga ggggcgactg gagcc atg gcg gag	174
	Met Ala Glu
	1

tcg gcg cct gct cgg cac agg aga aaa cga cgc tcc aca cct tta act	222
Ser Ala Pro Ala Arg His Arg Arg Lys Arg Arg Ser Thr Pro Leu Thr	
4 9 14 19	

tct tcc aca ctt cct tca caa gca aca gag aaa agc tcc tat ttt cag	270
Ser Ser Thr Leu Pro Ser Gln Ala Thr Glu Lys Ser Ser Tyr Phe Gln	
20 25 30 35	

acc acc gag att tca ctc tgg acg gtg gcc gct att cag gct gtg	318
Thr Thr Glu Ile Ser Leu Trp Thr Val Val Ala Ala Ile Gln Ala Val	
36 41 46 51	

gag aag aag atg gag tcc cag gct gcc cgg cta cag agc ctg gag ggg	366
Glu Lys Lys Met Glu Ser Gln Ala Ala Arg Leu Gln Ser Leu Glu Gly	
52 57 62 67	

cgc acg ggg aca gcc gag aag aag ctg gct gac tgc gag aag atg gcc	414
Arg Thr Gly Thr Ala Glu Lys Leu Ala Asp Cys Glu Lys Met Ala	
68 73 78 83	

gtg gag ttc ggg aac cag ctg gag ggc aag tgg gcc gtg ctg ggg acc	462
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<212> DNA  
<213> Homo sapiens
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 agttgtccct gtcacttggt gagtgtgtctc ttgttgcctg atatttaaa acgtttgata 120
 tcatttcaaa gctatagaaa aattgcaaaa acagtataag aaattctcat atacccttta 180
 cccaaatttg ccaagtgttt acattttcc ttgtttgcctt gttgatgacc atcaacccaaa 240
 taccaccagg aacataacctg taaccagaga cagctgattt gtagcttct gcagcaagga 300
 agctcacata ccacggcaca attctgcttt ccctggaaact gtgtcattca tgactctgca 360
 aattccctaa agtaggagga aaa atg acc atg tcc aag gag gca gtg acc 410
 Met Thr Met Ser Lys Glu Ala Val Thr
 1 5

ttc aag gat gtg gca gtg gtc ttc act gag gag gag ctg ggg ctg ctg		458
Phe Lys Asp Val Ala Val Val Phe Thr Glu Glu Glu Leu Gly Leu Leu		
10 15 20 25		
gac ctt gcc cag agg aag ctg tat cga gat gtg atg ctg gag aac ttc		506
Asp Leu Ala Gln Arg Lys Leu Tyr Arg Asp Val Met Leu Glu Asn Phe		
26 31 36 41		
agg aac ctg ctg tca gtg ggg cat caa cca ttc cac cga gat act ttc		554
Arg Asn Leu Leu Ser Val Gly His Gln Pro Phe His Arg Asp Thr Phe		
42 47 52 57		
cac ttt cta agg gag gaa aag ttt tgg atg atg gat ata gca acc caa		602
His Phe Leu Arg Glu Glu Lys Phe Trp Met Met Asp Ile Ala Thr Gln		
58 63 68 73		
aga gaa ggg aat tca gga ggc aag atc caa cct gag atg aag act ttt		650
Arg Glu Gly Asn Ser Gly Gly Lys Ile Gln Pro Glu Met Lys Thr Phe		
74 79 84 89		
cca gaa gca gga cca cat gaa ggg tgg tcc tgc cag cag atc tgg gaa		698
Pro Glu Ala Gly Pro His Glu Gly Trp Ser Cys Gln Gln Ile Trp Glu		
90 95 100 105		
gaa att gca agt gat tta acc agg cct caa gac tct acc ata aag agc		746
Glu Ile Ala Ser Asp Leu Thr Arg Pro Gln Asp Ser Thr Ile Lys Ser		
106 111 116 121		
tct cag ttc ttt gaa cag ggt gat gcc cac tcc cag gtt gag gaa gga		794
Ser Gln Phe Phe Glu Gln Gly Asp Ala His Ser Gln Val Glu Glu Gly		
122 127 132 137		
ata tct ata atg cac aca gga cag aaa cct tcc aat tgt ggg aag agt		842
Ile Ser Ile Met His Thr Gly Gln Lys Pro Ser Asn Cys Gly Lys Ser		
138 143 148 153		
aaa caa tcc ttc agt gat atg tcc atc ttt gat ctt cct cag caa ata		890
Lys Gln Ser Phe Ser Asp Met Ser Ile Phe Asp Leu Pro Gln Gln Ile		
154 159 164 169		
cgc tca gca gag aag tct cat tcc tgt gat gag tgt gga aaa agc ttc		938
Arg Ser Ala Glu Lys Ser His Ser Cys Asp Glu Cys Gly Lys Ser Phe		
170 175 180 185		
tgt tac atc tca gca ctt cat att cat cag aga gtc cac ctg gga gag		986
Cys Tyr Ile Ser Ala Leu His Ile His Gln Arg Val His Leu Gly Glu		
186 191 196 201		
aaa ctc ttt aag tgt gac gtg tgt ggt aag gaa ttc agt cag agt tta		1034
Lys Leu Phe Lys Cys Asp Val Cys Gly Lys Glu Phe Ser Gln Ser Leu		
202 207 212 217		
cat ctg caa act cat cag aga gtc cat act gga gag aaa cct ttc aaa		1082
His Leu Gln Thr His Gln Arg Val His Thr Gly Glu Lys Pro Phe Lys		
218 223 228 233		

tgt gaa caa tgt ggg aga ggc ttc aga tgt aga tca gca ctt aca gtt		1130
Cys Glu Gln Cys Gly Arg Gly Phe Arg Cys Arg Ser Ala Leu Thr Val		
234 239 244 249		
cat tgc aaa tta cac atg gga gag aaa cat tat aat tgt gag gca tgt		1178
His Cys Lys Leu His Met Gly Glu Lys His Tyr Asn Cys Glu Ala Cys		
250 255 260 265		
ggg agg gcc ttc att cat gat ttc cag ctt cag aaa cat cag aga att		1226
Gly Arg Ala Phe Ile His Asp Phe Gln Leu Gln Lys His Gln Arg Ile		
266 271 276 281		
cat act ggg gag aag cca ttc aaa tgt gaa ata tgt ggt aag agc ttc		1274
His Thr Gly Glu Lys Pro Phe Lys Cys Glu Ile Cys Gly Lys Ser Phe		
282 287 292 297		
tgt ctt agg tca agt ctt aat agg cat tgc atg gtc cac aca gca gag		1322
Cys Leu Arg Ser Ser Leu Asn Arg His Cys Met Val His Thr Ala Glu		
298 303 308 313		
aaa ctg tac aaa tct gaa aag tat gga aga ggt ttc att gat agg cta		1370
Lys Leu Tyr Lys Ser Glu Lys Tyr Gly Arg Gly Phe Ile Asp Arg Leu		
314 319 324 329		
gat ttg cat aag cat cag atg att cat atg gga cag aaa cca tat aat		1418
Asp Leu His Lys His Gln Met Ile His Met Gly Gln Lys Pro Tyr Asn		
330 335 340 345		
tgt aaa gaa tgt ggg aag agc ttc aaa tgg tcc tca tat ctt ttg gtc		1466
Cys Lys Glu Cys Gly Lys Ser Phe Lys Trp Ser Ser Tyr Leu Leu Val		
346 351 356 361		
cat caa cga gtc cac act gga gaa aag cca tac aaa tgt gag gag tgt		1514
His Gln Arg Val His Thr Gly Glu Lys Pro Tyr Lys Cys Glu Glu Cys		
362 367 372 377		
ggg aag ggc tac att agt aag tca ggt ctt gac ttg cac cat aga gcc		1562
Gly Lys Gly Tyr Ile Ser Lys Ser Gly Leu Asp Leu His His Arg Ala		
378 383 388 393		
cac aca gga gag aga cct tat aac tgt gat gac tgt ggg aag agc ttt		1610
His Thr Gly Glu Arg Pro Tyr Asn Cys Asp Asp Cys Gly Lys Ser Phe		
394 399 404 409		
aga cag gcc tca agt att ttg aat cat aag aga ctc cat tgc cga aaa		1658
Arg Gln Ala Ser Ser Ile Leu Asn His Lys Arg Leu His Cys Arg Lys		
410 415 420 425		
aaa cca ttc aaa tgt gag gat tgt gga aag aag ctt gta tac cgg tca		1706
Lys Pro Phe Lys Cys Glu Asp Cys Gly Lys Lys Leu Val Tyr Arg Ser		
426 431 436 441		
tac cgt aaa gac caa caa aaa aac cac agt gga gaa aat cca tcc aaa		1754
Tyr Arg Lys Asp Gln Gln Lys Asn His Ser Gly Glu Asn Pro Ser Lys		
442 447 452 457		
tgt gaa gac tgt ggg aag cgc tac aag agg cgc ttg aat ctt gat ata		1802

Cys Glu Asp Cys Gly Lys Arg Tyr Lys Arg Arg Leu Asn Leu Asp Ile
458 463 468 473

att tta tca tta ttt tta aat gac acg taa 1832
Ile Leu Ser Leu Phe Leu Asn Asp Thr *
474 479

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<212> DNA
<213> Homo sapiens

<220>
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<222> (135)..(1988)

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ggacctactc tcggaaccct caacgagcta gcgatagatt tagagggaaag gaagcaccgt 120

cggaaagcaa aggc atg att tca cct tca ctt gaa ctg ctt cat tca gga 170
Met Ile Ser Pro Ser Leu Glu Leu Leu His Ser Gly
1 5 10

ctc tgc aaa ttc cct gaa gta gaa gga aaa atg acc aca ttc aaa gag 218
Leu Cys Phe Pro Glu Val Glu Gly Lys Met Thr Thr Phe Lys Glu
13 18 23 28

gca gtg aca ttc aag gat gtg gct gtc ttc act gag gag gag ctg 266
Ala Val Thr Phe Lys Asp Val Ala Val Val Phe Thr Glu Glu Glu Leu
29 34 39 44

ggg ctg ctg gac cct gcc cag agg aag ctg tac cga gat gtg atg cta 314
Gly Leu Leu Asp Pro Ala Gln Arg Lys Leu Tyr Arg Asp Val Met Leu
45 50 55 60

gag aac ttc agg aac ctg ctc tca gta ggg aat caa cca ttc cac caa 362
Glu Asn Phe Arg Asn Leu Leu Ser Val Gly Asn Gln Pro Phe His Gln
61 66 71 76

gat act ttc cac ttc tta ggg aag gaa aag ttt tgg aag atg aag aca 410
Asp Thr Phe His Phe Leu Gly Lys Glu Lys Phe Trp Lys Met Lys Thr
77 82 87 92

aca agc caa aga gaa ggg aat tca gga ggc aag atc caa att gag atg 458
Thr Ser Gln Arg Glu Gly Asn Ser Gly Gly Lys Ile Gln Ile Glu Met
93 98 103 108

gag act gtt cca gaa gca gga cca cat gaa gag tgg tcc tgt cag caa 506
Glu Thr Val Pro Glu Ala Gly Pro His Glu Glu Trp Ser Cys Gln Gln
109 114 119 124

ata tgg gaa caa att gca agt gac cta acc agg tct caa aac tcc ata Ile Trp Glu Gln Ile Ala Ser Asp Leu Thr Arg Ser Gln Asn Ser Ile 125 130 135 140	554
agg aac agc tct cag ttc ttc aaa gaa ggt gat gtc ccc tgc cag att Arg Asn Ser Ser Gln Phe Phe Lys Glu Gly Asp Val Pro Cys Gln Ile 141 146 151 156	602
gag gca aga cta tct ata agt cac gtg caa cag aaa cct tac cgt tgt Glu Ala Arg Leu Ser Ile Ser His Val Gln Gln Lys Pro Tyr Arg Cys 157 162 167 172	650
aat gaa tgt aaa cag tcc atc agt gat gtt tct gtc ttt gat ctt cat Asn Glu Cys Lys Gln Ser Ile Ser Asp Val Ser Val Phe Asp Leu His 173 178 183 188	698
caa caa tca cac tca gga gag aaa tct cat aca tgt ggt gag tgt gga Gln Gln Ser His Ser Gly Glu Lys Ser His Thr Cys Gly Glu Cys Gly 189 194 199 204	746
aaa agc ttc tgt tac agc cca gcc ctt cat att cat cag aga gtc cat Lys Ser Phe Cys Tyr Ser Pro Ala Leu His Ile His Gln Arg Val His 205 210 215 220	794
atg gga gaa aaa tgc tat aag tgt gat gtg tgt ggt aag gaa ttt aat Met Gly Glu Lys Cys Tyr Lys Cys Asp Val Cys Gly Lys Glu Phe Asn 221 226 231 236	842
cag agc tca cat ctg caa act cat cag aga gtc cat act gga gag aaa Gln Ser Ser His Leu Gln Thr His Gln Arg Val His Thr Gly Glu Lys 237 242 247 252	890
cca ttc aaa cgt ggg caa tgt ggg aaa ggc ttc cat agt aga tca gca Pro Phe Lys Arg Gly Gln Cys Gly Lys Gly Phe His Ser Arg Ser Ala 253 258 263 268	938
ctt aat gtt cat tgc aaa ttg cac aca gga gag aaa cct tat aat tgt Leu Asn Val His Cys Lys Leu His Thr Gly Glu Lys Pro Tyr Asn Cys 269 274 279 284	986
gag gaa tgt ggg aaa gcc ttc att cat gat tca cag ctc cag gaa cat Glu Glu Cys Gly Lys Ala Phe Ile His Asp Ser Gln Leu Gln Glu His 285 290 295 300	1034
cag aga atc cat act ggg gag aag cca ttc aaa tgt gat ata tgt ggt Gln Arg Ile His Thr Gly Glu Lys Pro Phe Lys Cys Asp Ile Cys Gly 301 306 311 316	1082
aag agc ttc cgt gtt aga tca aga ctt aat agg cat tcc atg gtt cac Lys Ser Phe Arg Val Arg Ser Arg Leu Asn Arg His Ser Met Val His 317 322 327 332	1130
aca gga gaa aaa cca ttc aga tgt gat aca tgt ggc aag aac ttt cgt Thr Gly Glu Lys Pro Phe Arg Cys Asp Thr Cys Gly Lys Asn Phe Arg 333 338 343 348	1178
cag aga tca gca ctt aat agt cat tcc atg gtc cac ata gaa gag aag	1226

Gln Arg Ser Ala Leu Asn Ser His Ser Met Val His Ile Glu Glu Lys			
349	354	359	364
cca tac aaa tgt gag caa tgt gga aaa ggc ttc att tgt agg cga gat			1274
pro Tyr Lys Cys Glu Gln Cys Gly Lys Gly Phe Ile Cys Arg Arg Asp			
365	370	375	380
ttt tgt aag cat cag atg gtc cac aca gga gag aaa cca tat aat tgt			1322
Phe Cys Lys His Gln Met Val His Thr Gly Glu Lys Pro Tyr Asn Cys			
381	386	391	396
aaa gaa tgt ggg aag acc ttc aga tgg tcc tca tgt ctt ttg aac cat			1370
Lys Glu Cys Gly Lys Thr Phe Arg Trp Ser Ser Cys Leu Leu Asn His			
397	402	407	412
cag caa gtc cac agt gga caa aaa tcc ttc aaa tgt gaa gaa tgt ggg			1418
Gln Gln Val His Ser Gly Gln Lys Ser Phe Lys Cys Glu Glu Cys Gly			
413	418	423	428
aag gga ttt tat aca aat tca cga cga tct tcc cat cag aga tcc cac			1466
Lys Gly Phe Tyr Thr Asn Ser Arg Arg Ser Ser His Gln Arg Ser His			
429	434	439	444
aat gga gaa aag cca tat aac tgt gag gag tgt ggt aag gac tat aaa			1514
Asn Gly Glu Lys Pro Tyr Asn Cys Glu Glu Cys Gly Lys Asp Tyr Lys			
445	450	455	460
agg agg ttg gat ctt gag ttt cac cag agg gtc cac acg ggt gag aga			1562
Arg Arg Leu Asp Leu Glu Phe His Gln Arg Val His Thr Gly Glu Arg			
461	466	471	476
ccc tat aat tgt aag gaa tgt ggc aag agc ttt ggc tgg gcc tcc tgt			1610
Pro Tyr Asn Cys Lys Glu Cys Gly Lys Ser Phe Gly Trp Ala Ser Cys			
477	482	487	492
ctt ttg aaa cat cag aga ctc cac agt ggg gaa aaa cct ttc aaa tgt			1658
Leu Leu Lys His Gln Arg Leu His Ser Gly Glu Lys Pro Phe Lys Cys			
493	498	503	508
gaa gag tgt gga aag aga ttt act cag agt aca caa ctt cat tcc cat			1706
Glu Glu Cys Gly Lys Arg Phe Thr Gln Ser Thr Gln Leu His Ser His			
509	514	519	524
cag aca tgc cat act gga gaa aag cta tac aaa tgt gag cag tgt gag			1754
Gln Thr Cys His Thr Gly Glu Lys Leu Tyr Lys Cys Glu Gln Cys Glu			
525	530	535	540
aag ggg tac aac agt aaa ttt aat ctt gac atg cac cag agg gtc cac			1802
Lys Gly Tyr Asn Ser Lys Phe Asn Leu Asp Met His Gln Arg Val His			
541	546	551	556
agg gga gag cga ccc tat aat tgt aag gaa tgt gga aag agc ttt ggc			1850
Arg Gly Glu Arg Pro Tyr Asn Cys Lys Glu Cys Gly Lys Ser Phe Gly			
557	562	567	572
tgg gct tca tgt ctt ttg aaa cat cag aga ctc cac agt gga gaa aag			1898
Trp Ala Ser Cys Leu Leu Lys His Gln Arg Leu His Ser Gly Glu Lys			

573	578	583	588	
cca ttg aaa tct gga gtg tgg gaa gag atc tac tca gaa ttc aca gct				1946
Pro Leu Lys Ser Gly Val Trp Glu Glu Ile Tyr Ser Glu Phe Thr Ala				
589	594	599	604	

tca ttt aca tca gta agt cta tgt ggg aga aaa gcc ata taa				1988
Ser Phe Thr Ser Val Ser Leu Cys Gly Arg Lys Ala Ile *				
605	610	615		

<210> 1081
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<220>
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 <222> (1)..(1677)
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aacggcgcga ggtgaaggga ggtgacggag tgtgcccgcg cgccgcggggg tccccctcagt 180

cccagcagtt cccttcgtgc gcggggggcg gcgagggtct tcagcagtcg ggagaggccc 240

ttgacggcgc c atg tcg gcg ggc ggt cca tgc cca gca gca gcc gga ggg 290
 Met Ser Ala Gly Gly Pro Cys Pro Ala Ala Ala Gly Gly
 1 5 10

ggc cca ggg ggc gcc tcc tgc tcc gtg ggg gcc cct ggc ggg gta tcc 338
 Gly Pro Gly Gly Ala Ser Cys Ser Val Gly Ala Pro Gly Gly Val Ser
 14 19 24 29

atg ttc cgg tgg ctg gag gtg ctg gag aag gag ttc gac aaa gct ttt 386
 Met Phe Arg Trp Leu Glu Val Leu Glu Lys Glu Phe Asp Lys Ala Phe
 30 35 40 45

gtg gat gtg gat ctg ctc ctg gga gag atc gat cca gac caa gcg gac 434
 Val Asp Val Asp Leu Leu Leu Gly Glu Ile Asp Pro Asp Gln Ala Asp
 46 51 56 61

atc act tat gag ggg cga cag aag atg acc agc ctg agc tcc tgc ttt 482
 Ile Thr Tyr Glu Gly Arg Gln Lys Met Thr Ser Leu Ser Ser Cys Phe
 62 67 72 77

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78 83 88 93	
ctg gag gca cag ttg gtg gat ctg aaa tct gaa ctg aca gaa acc caa Leu Glu Ala Gln Leu Val Asp Leu Lys Ser Glu Leu Thr Glu Thr Gln	578
94 99 104 109	
gca gag aaa gtt gtt ttg gag aaa gaa gta cat gat cag ctt tta cag Ala Glu Lys Val Val Leu Glu Lys Glu Val His Asp Gln Leu Leu Gln	626
110 115 120 125	
ctg cac tct att cag ctg cag ctt cat gct aaa act ggt caa agt gct Leu His Ser Ile Gln Leu Gln Leu His Ala Lys Thr Gly Gln Ser Ala	674
126 131 136 141	
gac tct ggt acc att aag gca aaa ttg gaa aga gag ctt gag gca aac Asp Ser Gly Thr Ile Lys Ala Lys Leu Glu Arg Glu Leu Glu Ala Asn	722
142 147 152 157	
aaa aaa gaa aaa atg aaa gaa gca caa ctt gaa gct gaa gtg aaa ttg Lys Lys Glu Lys Met Lys Glu Ala Gln Leu Glu Ala Glu Val Lys Leu	770
158 163 168 173	
ttg aga aaa gag aat gaa gcc ctt cgt aga cat ata gct gtt ctc cag Leu Arg Lys Glu Asn Glu Ala Leu Arg Arg His Ile Ala Val Leu Gln	818
174 179 184 189	
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190 195 200 205	
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206 211 216 221	
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222 227 232 237	
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238 243 248 253	
ttg aaa cga cca atg caa gca cca ggc cat gat caa gat tcc cta Leu Lys Arg Pro Met Gln Ala Pro Pro Gly His Asp Gln Asp Ser Leu	1058
254 259 264 269	
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ccaccggact tggatcgag cagccttcag gggacgtggc gcagtcgaac agagccacc	359
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atg ggg acg acg gcc cca ggg ccc att cac ctg ctg gag cta tgt gac	407
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1 5 10 15

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Gln Lys Leu Met Glu Phe Leu Cys Asn Met Asp Asn Lys Asp Leu Val
17 22 27 32

tgg ctt gag gaa atc caa gag gag gcc gag cgc atg ttc acc aga gaa	503
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Trp Leu Glu Glu Ile Gln Glu Glu Ala Glu Arg Met Phe Thr Arg Glu
33 38 43 48

ttc agc aaa gag cca gag ctg atg ccc aaa aca cct tct cag aag aac	551
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Phe Ser Lys Glu Pro Glu Leu Met Pro Lys Thr Pro Ser Gln Lys Asn
49 / 54 59 64

cga cgg aag aag aga cgg att tct tat gtt cag gat gaa aac aga gat	599
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Arg Arg Lys Lys Arg Arg Ile Ser Tyr Val Gln Asp Glu Asn Arg Asp

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Pro Ile Arg Arg Arg Leu Ser Arg Arg Lys Ser Arg Ser Ser Gln Leu					
81	86	91	96		
agc tcc cga cgc ctc cgc agc aag gac agt gta gag aag ctg gct aca					695
Ser Ser Arg Arg Leu Arg Ser Lys Asp Ser Val Glu Lys Leu Ala Thr					
97	102	107	112		
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Val Val Gly Glu Asn Gly Ser Val Leu Arg Arg Val Thr Arg Ala Ala					
113	118	123	128		
gct gca gct gcc gcg gct acc atg gca ttg gct gca cct tct tca ccc					791
Ala Ala Ala Ala Ala Ala Thr Met Ala Leu Ala Ala Pro Ser Ser Pro					
129	134	139	144		
acc cct gag tct ccc acg atg ctg act aag aag ccc gag gat aac cac					839
Thr Pro Glu Ser Pro Thr Met Leu Thr Lys Lys Pro Glu Asp Asn His					
145	150	155	160		
acc cag tgc cag ctg gtg cct gtg gag atc ggc atc agt gag cgc					887
Thr Gln Cys Gln Leu Val Pro Val Val Glu Ile Gly Ile Ser Glu Arg					
161	166	171	176		
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Gln Asn Ala Glu Gln His Val Thr Gln Leu Met Ser Thr Glu Pro Leu					
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ccc cgc act ctg tcc ccg act cca gct tca gcc aca gct cca acc tcc					983
Pro Arg Thr Leu Ser Pro Thr Pro Ala Ser Ala Thr Ala Pro Thr Ser					
193	198	203	208		
cag ggc atc ccg aca tca gat gag gaa tca aca cct aag aag tcg aag					1031
Gln Gly Ile Pro Thr Ser Asp Glu Glu Ser Thr Pro Lys Lys Ser Lys					
209	214	219	224		
gcc agg ata ctg gag tcc atc aca gtg agc tcc ctg atg gct aca ccc					1079
Ala Arg Ile Leu Glu Ser Ile Thr Val Ser Ser Leu Met Ala Thr Pro					
225	230	235	240		
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Gln Asp Pro Lys Gly Gln Gly Val Gly Thr Gly Arg Ser Ala Ser Lys					
241	246	251	256		
ctc agg att gc ^g cag gtc tcc cct ggc cca cgg gac tcg cca gcc ttt					1175
Leu Arg Ile Ala Gln Val Ser Pro Gly Pro Arg Asp Ser Pro Ala Phe					
257	262	267	272		
cca gat tct cca tgg cgg gag cgg gtg ctg gct ccc atc ctg ccg gat					1223
Pro Asp Ser Pro Trp Arg Glu Arg Val Leu Ala Pro Ile Leu Pro Asp					
273	278	283	288		
aac ttc tcc acg ccc acg ggc tct cgc acg gac tct caa tcg gtg cgg					1271
Asn Phe Ser Thr Pro Thr Gly Ser Arg Thr Asp Ser Gln Ser Val Arg					
289	294	299	304		

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aag tac tct ctg gtg gcc aaa cag gaa agt gtt gtc cgc agg gcg agc Lys Tyr Ser Leu Val Ala Lys Gln Glu Ser Val Val Arg Arg Ala Ser 321 326 331 336	1367
aga agg ctt gcc aag aag act gcc gaa gag cca gct gcc tct ggc cgc Arg Arg Leu Ala Lys Lys Thr Ala Glu Glu Pro Ala Ala Ser Gly Arg 337 342 347 352	1415
atc atc tgt gag tct ggg ggc ttg gca gtg gcg ggt ggt cct tgg tgc Ile Ile Cys Glu Ser Gly Gly Leu Ala Val Ala Gly Gly Pro Trp Cys 353 358 363 368	1463
cag gct cag atg gag gct ttc tga gggatcatct agcaaggagc tgtccagaga Gln Ala Gln Met Glu Ala Phe *369 374	1517
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tcg gtg aag gtg gcg gtg cgg gtc cgc ccc ttc aat tcc cgg gaa atg Ser Val Lys Val Ala Val Arg Val Arg Pro Phe Asn Ser Arg Glu Met 5 10 15 20 /	221
agc cgt gac tcc aag tgc atc att cag atg tct gga agc acc acc acc	269

Ser	Arg	Asp	Ser	Lys	Cys	Ile	Ile	Gln	Met	Ser	Gly	Ser	Thr	Thr	Thr	
21					26				31					36		
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37					42				47					52		
gac tac tcc tac tgg gcg cac acc tca cct gag gac atc aac tac gcg Asp Tyr Ser Tyr Trp Ala His Thr Ser Pro Glu Asp Ile Asn Tyr Ala															365	
53					58				63					68		
tcg caa aag cag gtg tac cgg gac atc ggc gag gag atg ctg cag cat Ser Gln Lys Gln Val Tyr Arg Asp Ile Gly Glu Glu Met Leu Gln His															413	
69					74				79					84		
gcc ttt gag gga tac aac gtg tgc atc ttc gcc tat ggg cag acg ggt Ala Phe Glu Gly Tyr Asn Val Cys Ile Phe Ala Tyr Gly Gln Thr Gly															461	
85					90				95					100		
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101					106				111					116		
ggc atc atc cca cag ctc tgc gag gac ctc ttc tct cgg atc aac gac Gly Ile Ile Pro Gln Leu Cys Glu Asp Leu Phe Ser Arg Ile Asn Asp															557	
117					122				127					132		
acg acc aac gac aac atg tcc tac tcc gtg gag gtc agc tac atg gag Thr Thr Asn Asp Asn Met Ser Tyr Ser Val Glu Val Ser Tyr Met Glu															605	
133					138				143					148		
att tac tgt gag cgc gtc cgt gac ctc ctg aac ccc aag aac aag ggc Ile Tyr Cys Glu Arg Val Arg Asp Leu Leu Asn Pro Lys Asn Lys Gly															653	
149					154				159					164		
aac ctt cgc gtg agg gag cac cca ctg ctg ggg ccc tac gtg gag gac Asn Leu Arg Val Arg Glu His Pro Leu Leu Gly Pro Tyr Val Glu Asp															701	
165					170				175					180		
ctc tcc aag ctg gct gtc acc tcc tac aat gac atc cag gac ctc atg Leu Ser Lys Leu Ala Val Thr Ser Tyr Asn Asp Ile Gln Asp Leu Met															749	
181					186				191					196		
gac tca ggg aac aag gcc agg acc gtg gcg gcc acc aac atg aat gag Asp Ser Gly Asn Lys Ala Arg Thr Val Ala Ala Thr Asn Met Asn Glu															797	
197					202				207					212		
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213					218				223					228		
cgc cat gac gca gag acc aat atc acc acg gag aag gtg agc aaa atc Arg His Asp Ala Glu Thr Asn Ile Thr Thr Glu Lys Val Ser Lys Ile															893	
229					234	/			239					244		
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245	250	255	260	
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acc ctg ggc aag gtc atc tcc gcc ctg gct gaa atg gac tcc gga ccc Thr Leu Gly Lys Val Ile Ser Ala Leu Ala Glu Met Asp Ser Gly Pro 277 282 287 292				1037
aac aag aac aag aaa aag aag aca gat ttc att ccg tac cga gat Asn Lys Asn Lys Lys Lys Thr Asp Phe Ile Pro Tyr Arg Asp 293 298 303 308				1085
tcc gtg ttg acc tgg ctc ctc cgg gaa aac ctg ggc ggt aac tca agg Ser Val Leu Thr Trp Leu Leu Arg Glu Asn Leu Gly Gly Asn Ser Arg 309 314 319 324				1133
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Met Gln Tyr Ser His His Cys Glu His
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Cys Thr Ile Val Ile Gly Glu Phe Gln Phe Lys Ala His Arg Asn Val
26 31 36 41

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Leu Ala Ser Phe Ser Glu Tyr Phe Gly Ala Ile Tyr Arg Ser Thr Ser
42 47 52 57

gag aac aat gtc ttt ctt gat cag agt cag gtg aag gct gat gga ttt 305
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58 63 68 73

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Gln Lys Leu Leu Glu Phe Ile Tyr Thr Gly Thr Leu Asn Leu Asp Ser
74 79 84 89

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122 127 132 137

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Gln Ala Ser Thr Leu Thr Tyr His Val Arg Arg Ala Leu Leu Gly Glu			
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Ser Leu Ile Thr His Ser Arg Lys His Thr Gly Glu Lys Pro Tyr Ile			
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Cys Gly Ile Cys Gly Lys Ser Phe Ile Ser Ser Gly Glu Leu Asn Lys			
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Thr Leu Ser Glu Gln Asp Ser Ile Gln Lys Ser Pro Leu Ser Glu Thr			
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Met Asp Val Lys Pro Ser Asp Met Thr Leu Pro Leu Ala Leu Pro Leu			
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Gly Thr Glu Asp His His Met Leu Leu Pro Val Thr Asp Thr Gln Ser			
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cct aca tca gat aca ttg ttg agg tca act gtg aat ggg tat tca gaa			1889
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Cys Ala Glu Pro Ser Glu Pro Ser Ala Pro Leu Pro Ala Gly Val Pro

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tgt ttg cac aag agc cga att gca gat ttg cag gat gtc ctg aag gag						103
Cys Leu His Lys Ser Arg Ile Ala Asp Leu Gln Asp Val Leu Lys Glu						
3	8		13		18	
ccc tca att gca ttg gaa aag ctg cgg gaa ctc agc ttt agt ggc atc						151
Pro Ser Ile Ala Leu Glu Lys Leu Arg Glu Leu Ser Phe Ser Gly Ile						
19	24		29		34	
ccc tgt gag ggc gga ctg cgg tgc ctc tgc tgg aag att ctc ttg aac						199
Pro Cys Glu Gly Leu Arg Cys Leu Cys Trp Lys Ile Leu Leu Asn						
35	40		45		50	
tac ctt ccc ttg gag agg gcc tca tgg acc tcc atc ctg gcc aag cag						247
Tyr Leu Pro Leu Glu Arg Ala Ser Trp Thr Ser Ile Leu Ala Lys Gln						
51	56		61		66	
agg gag ctg tat gcc cag ttc ctg agg gaa atg atc atc cag cct ggc						295
Arg Glu Leu Tyr Ala Gln Phe Leu Arg Glu Met Ile Ile Gln Pro Gly						
67	72		77		82	
att gcc aag gcc aac atg ggt gtg tcc agg gag gat gtg act ttt gag						343
Ile Ala Lys Ala Asn Met Gly Val Ser Arg Glu Asp Val Thr Phe Glu						
83	88		93		98	
gac cat tca ctc aac ccc aac cct gac agc cgg tgg aac acg tac ttc						391
Asp His Ser Leu Asn Pro Asn Pro Asp Ser Arg Trp Asn Thr Tyr Phe						
99	104		109		114	
aag gac aac gag gtg ctg cag atc gac aaa gat gtc cgg tag g						437
Lys Asp Asn Glu Val Leu Leu Gln Ile Asp Lys Asp Val Arg *						
115	120		125			

<210> 1087

<211> 2576

<212> DNA

<213> Homo sapiens

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<222> (1716)..(1856)

<400> 1087

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ctttaccttc	tttgcagact	ttgggttgggt	gaggctgtgg	aatggaaaca	ggcttgagaa	480
acaggaatgg	tagtgcatt	ggccttccag	tcccacctat	cacagcctta	atcaccccgag	540
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tcctttttt	catctacctg	ttgggttgctc	tttcattca	gtacatcaac	atttataaaa	660
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atctaaacctt cagtttactt taatagaaaa gaaaa atg gtc tgg atg tca ctt Met Val Trp Met Ser Leu	1733
1	
ggg ccc aaa atc ttt tgg tac att tta gtg ccc ttt ctt cac cca ttc Gly Pro Lys Ile Phe Trp Tyr Ile Leu Val Pro Phe Leu His Pro Phe	1781
7 12 17 22	
aga agt act tct gca gct gga atg gtc ctt cag aga aca ctc agt tct Arg Ser Thr Ser Ala Ala Gly Met Val Leu Gln Arg Thr Leu Ser Ser	1829
23 28 33 38	
tct aga aag gag aca ctt aaa ata taa ttgcc tctccctccc atccctaact Ser Arg Lys Glu Thr Leu Lys Ile *	1881
39 44	
catacagcca gaaagtcaagg ttgaaggatt gtggaggact ctgctcttga acttttctgc	1941
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gtatctcatg cccgccttta tttcttattt catcgaccat taaggctgtt aaatctgctc	2421
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 <211> 826
 <212> DNA
 <213> Homo sapiens

<220> /
 <221> CDS /
 <222> (529)..(795)

<400> 1088

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tgcacacccg gaagcagatc gcgcggggaa aagatcacag cgctgcgcgt cagttccgt	180
ctacctggac taaacatttg ctgcggcccg tctgcctgaa tcgaacgtgc acttggcagt	240
cttcccttgt ccataccgt ttcctgggaa tcgctacgga ccttaaaata ccagcaacag	300
ccccctcgcc ccaaggtctt gctctgtcag actagagtac agtgcctgatca tctccgctca	360
ctgcagcctc aacctcctgg gctcaagcag tcttctgccc tcagagtgc gggattacag	420
acgggagcca ccacgccagg cctacgagat ttgacttgta aagaattaat tatattgact	480
gagagagaag cccagaagag gaagaagagg aaagaaaagg agtcaggg atg gct ctt	537
	Met Ala Leu
	1
aca cag gga cct ttg aca ttc agg gat gta gcc ata gaa ttc tct cag	585
Thr Gln Gly Pro Leu Thr Phe Arg Asp Val Ala Ile Glu Phe Ser Gln	
4 9 14 19	
gag gag tgg aaa tcc ctg gac cct gtg cag aaa gct ttg tac tgg gat	633
Glu Glu Trp Lys Ser Leu Asp Pro Val Gln Lys Ala Leu Tyr Trp Asp	
20 25 30 35	
gtg atg ttg gag aac tac agg aac ctg gtc ttc ctg ggt aag gat aat	681
Val Met Leu Glu Asn Tyr Arg Asn Leu Val Phe Leu Gly Lys Asp Asn	
36 41 46 51	
ttt gct cta gaa gtt aag atc tgc cct cgt gta ttt ttg tat ttt ctc	729
Phe Ala Leu Glu Val Lys Ile Cys Pro Arg Val Phe Leu Tyr Phe Leu	
52 57 62 67	
tgt tgt ctt tct tgg gag ccc ttc cat tat ttg act gag act gaa gcc	777
Cys Cys Leu Ser Trp Glu Pro Phe His Tyr Leu Thr Glu Thr Glu Ala	
68 73 78 83	
ttg ttg act cac aaa taa aaagcttcat aatgctgaaa aaaaaaaaaa a	826
Leu Leu Thr His Lys *	
84 89	

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 Met Arg Lys His Leu Ser Trp Trp Trp Leu Ala Thr Val Cys Met
 1 5 10

ctg ctc ttc agc cac ctc tct gct cag acg agg ggc atc aag cac 157
 Leu Leu Phe Ser His Leu Ser Ala Val Gln Thr Arg Gly Ile Lys His
 16 21 26 31

aga atc aag tgg aac cgg aag gcc ctg ccc agc act gcc cag atc act 205
 Arg Ile Lys Trp Asn Arg Lys Ala Leu Pro Ser Thr Ala Gln Ile Thr
 32 37 42 47

gag gcc cag gtg gct gag aac cgc ccg gga gcc ttc atc aag caa ggc 253
 Glu Ala Gln Val Ala Glu Asn Arg Pro Gly Ala Phe Ile Lys Gln Gly
 48 53 58 63

cgc aag ctc gac att gac ttc gga gcc gag ggc aac agg tac tac gag 301
 Arg Lys Leu Asp Ile Asp Phe Gly Ala Glu Asn Arg Tyr Tyr Glu
 64 69 74 79

gcc aac tac tgg cag ttc ccc gat ggc atc cac tac aac ggc tgc tct 349
 Ala Asn Tyr Trp Gln Phe Pro Asp Gly Ile His Tyr Asn Gly Cys Ser
 80 85 90 95

gag gct aat gtg acc aag gag gca ttt gtc acc ggc tgc atc aat gcc 397
 Glu Ala Asn Val Thr Lys Glu Ala Phe Val Thr Gly Cys Ile Asn Ala
 96 101 106 111

acc cag gcg gcg aac cag ggg gag ttc cag aag cca gac aac aag ctc 445
 Thr Gln Ala Ala Asn Gln Gly Glu Phe Gln Lys Pro Asp Asn Lys Leu
 112 117 122 127

cac cag cag gtg ctc tgg cgg ctg cag gag ctc tgc tcc ctc aag 493
 His Gln Gln Val Leu Trp Arg Leu Val Gln Glu Leu Cys Ser Leu Lys
 128 133 138 143

cat tgc gag ttt tgg ttg gag agg ggc gca gga ctt cgg gtc acc atg 541
 His Cys Glu Phe Trp Leu Glu Arg Gly Ala Gly Leu Arg Val Thr Met
 144 149 154 159

cac cag cca gtg ctc ctc tgc ctt ctg gct ttg atc tgg ctc acg gtg 589
 His Gln Pro Val Leu Leu Cys Leu Leu Ala Leu Ile Trp Leu Thr Val
 160 165 170 175

aaa taa gcttgcagg aggctggcag tacagagtgc agcagcgagc aaatcctggc 645
 Lys *
 176

aagtgaccctt gctcttctcc cccaaaccca cgcgtttct gaaaagtgcggcc atgagcggcg 705
 atgcactctc actgcaaatg ccgctctcac gtatgcggcc tgttatgtgc ctgcgttctg 765 /

<210> 1090
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<212> DNA
<213> *Homo sapiens*

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<222> (197) . . (1672)

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 gcggc gctacccaagc cggcggtctc cggcaagcag ggcaatgtgc tcccgctctg 180
 acgag aagacc atg aac ctc aac ccc atg atc ctg acc aac atc 229
 Met Asn Leu Asn Pro Met Ile Leu Thr Asn Ile
 1 5
 cg tcg cct tac ttc aaa gta cag ctc tac gag ctc aag acc tac 277
 er Ser Pro Tyr Phe Lys Val Gln Leu Tyr Glu Leu Lys Thr Tyr
 17 22 27
 ag gtg gtg gac gag atc tac ttt aag gtc acg cac gtt gaa cca 325
 lu Val Val Asp Glu Ile Tyr Phe Lys Val Thr His Val Glu Pro
 33 38 43
 ag aaa gga agc agg aaa aca gcg ggc cag aca ggg atg tgc gga 373
 lu Lys Gly Ser Arg Lys Thr Ala Gly Gln Thr Gly Met Cys Gly
 49 54 59
 tt cga ggt gtt gga aca gga gga att gtt tct aca gca ttt tgc 421
 al Arg Gly Val Gly Thr Gly Ile Val Ser Thr Ala Phe Cys
 65 70 75
 ta tac aaa tta ttt acc ctg aag tta act cga aag caa gtg atg 469
 eu Tyr Lys Leu Phe Thr Leu Lys Leu Thr Arg Lys Gln Val Met
 81 86 91
 tt ata aca cac aca gac tct cca tat att aga gcg ctt gga ttt 517
 eu Ile Thr His Thr Asp Ser Pro Tyr Ile Arg Ala Leu Gly Phe
 97 102 107
 at ata aga tat aca cag ccc cct aca gat ctg tgg gac tgg ttt 565
 yr Ile Arg Tyr Thr Gln Pro Pro Thr Asp Leu Trp Asp Trp Phe
 113 118 123
 cc ttc ctt gat gat gaa gag gac cta gat gtg aag gct ggt gga 613
 er Phe Leu Asp Asp Glu Glu Asp Leu Asp Val Lys Ala Gly Gly
 129 134 139
 gt gta atg acc att gga gaa atg cta cga tct ttt ctc aca aaa 661
 ys Val Met Thr Ile Gly Glu Met Leu Arg Ser Phe Leu Thr Lys
 145 150 155

ctg gag tgg ttt tct acc ttg ttt cca aga att cca gtt cca gtt caa Leu Glu Trp Phe Ser Thr Leu Phe Pro Arg Ile Pro Val Pro Val Gln 156 161 166 171	709
aag aat att gat caa cag att aaa acc cga cct aga aaa atc aag aaa Lys Asn Ile Asp Gln Gln Ile Lys Thr Arg Pro Arg Lys Ile Lys Lys 172 177 182 187	757
gat ggg aag gaa ggt gct gag gaa ata gac aga cat gtt gaa cgc aga Asp Gly Lys Glu Gly Ala Glu Glu Ile Asp Arg His Val Glu Arg Arg 188 193 198 203	805
cgt tca agg tct cca agg aga tct ctg agt cca cgg agg tcc cca aga Arg Ser Arg Ser Pro Arg Arg Ser Leu Ser Pro Arg Arg Ser Pro Arg 204 209 214 219	853
agg tca aga agt aga agt cat cat cgg gag ggc cat ggg tct tct agt Arg Ser Arg Ser Arg Ser His His Arg Glu Gly His Gly Ser Ser Ser 220 225 230 235	901
ttt gac aga gaa tta gaa aga gag aaa gaa cgc cag cga cta gag cgt Phe Asp Arg Glu Leu Glu Arg Glu Lys Glu Arg Gln Arg Leu Glu Arg 236 241 246 251	949
gaa gcc aaa gaa agg gag aaa gaa cgg cga aga tcc cga agt att gag Glu Ala Lys Glu Arg Glu Lys Glu Arg Arg Arg Ser Arg Ser Ile Asp 252 257 262 267	997
cgg ggg tta gaa cgc agg cgc agc aga agt agg gaa agg cat aga agt Arg Gly Leu Glu Arg Arg Ser Arg Ser Arg Glu Arg His Arg Ser 268 273 278 283	1045
cgc agt cga agt cgt gat agg aaa ggg gat aga agg gac agg gat cga Arg Ser Arg Ser Arg Asp Arg Lys Gly Asp Arg Arg Asp Arg Asp Arg 284 289 294 299	1093
gaa aga gag aaa gaa aat gag aga ggt aga aga cga gat cgt gac tat Glu Arg Glu Lys Glu Asn Glu Arg Gly Arg Arg Asp Arg Asp Tyr 300 305 310 315	1141
gat aag gaa aga gga aat gaa cga gaa aaa gag aga gag cga tca aga Asp Lys Glu Arg Gly Asn Glu Arg Glu Lys Glu Arg Glu Arg Ser Arg 316 321 326 331	1189
gaa agg tcc aag gaa cag aga agt agg gga gag gta gaa gag aag aaa Glu Arg Ser Lys Glu Gln Arg Ser Arg Gly Glu Val Glu Glu Lys Lys 332 337 342 347	1237
cat aaa gaa gac aaa gat gat agg cgg cac aga gat gac aaa aga gat His Lys Glu Asp Lys Asp Asp Arg Arg His Arg Asp Asp Lys Arg Asp 348 353 358 363	1285
tcc aag aaa gag aaa aaa cac agt aga agc aga agc aga gaa agg aaa Ser Lys Lys Glu Lys Lys His Ser Arg Ser Arg Ser Arg Glu Arg Lys 364 369 374 379	1333
cac aga agt agg agt cga agt aga aat gca ggg aaa cga agt aga agt	1381

His Arg Ser Arg Ser Arg Ser Arg Asn Ala Gly Lys Arg Ser Arg Ser			
380	385	390	395
aga agc aaa gag aaa tca agt aaa cat aaa aat gaa agt aaa gaa aaa			1429
Arg Ser Lys Glu Lys Ser Ser Lys His Lys Asn Glu Ser Lys Glu Lys			
396	401	406	411
tca aat aaa cga agt cga agt ggc agt caa gga aga act gac agt gtt			1477
Ser Asn Lys Arg Ser Arg Ser Gly Ser Gln Gly Arg Thr Asp Ser Val			
412	417	422	427
gaa aaa tca aaa aaa cgg gaa cat agt ccc agc aaa gaa aaa tct aga			1525
Glu Lys Ser Lys Lys Arg Glu His Ser Pro Ser Lys Glu Lys Ser Arg			
428	433	438	443
aag cgt agt aga agc aaa gaa cgt tcc cac aaa cga gat cac agt gat			1573
Lys Arg Ser Arg Ser Lys Glu Arg Ser His Lys Arg Asp His Ser Asp			
444	449	454	459
agt aag gac cag tca gac aaa cat gat cgt cga agg agc caa agt ata			1621
Ser Lys Asp Gln Ser Asp Lys His Asp Arg Arg Ser Gln Ser Ile			
460	465	470	475
gaa caa gag agc caa gaa aaa cag cat aaa aac aaa gat gag act gtg			1669
Glu Gln Glu Ser Gln Glu Lys Gln His Lys Asn Lys Asp Glu Thr Val			
476	481	486	491
tga aaat attttgtaaa agtggatcac attgaatcct ataaatgatt aaatctgctt			1726
*			
492			
ttttccccca cggttagatt gtgcagtagt tcgcactcct caagctctcc ctgtaggctg			1786
cattttcatt tcctcttcg tggatggaaat tgcccttgta attccattta ttgcattgg			1846
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aaaa			2030

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 <213> Homo sapiens

<220>
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 <222> (630)..(950)

<400> 1091

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ttaatgttt tccttaatac tcaagtgatg tttgtctcta gtgttctaat gtagcacaaa	1297
tcctatgtaa aatcatacta tgtatTTTG acattaatgt tgaaatcaaa tatatgcaca	1357
agtctttaat ttgtgtaat gtgttaagtg ctgttcattt aagttatgaa aaatgagaat	1417
aaaacg	1423

<210> 1092
 <211> 1243
 <212> DNA
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<220>
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 <222> (319) ... (891)

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tagtcgattt ctgtgaaaac gccccggttt ctgccaaagg gcaggagtcg ctgctttgt	180
gccgggtgct gctgggtgtg tagggcgctg ttgcttttt aaggacgctc tgcactgaat	240
taggcttcct cgtgggtcat gatcagttaa gtcctgtcaa agaaaaaagg actgagtgca	300
gaagaaaaaga gaactcgc atg atg gaa ata ttt tct gaa aca aaa gat gta	351
Met Met Glu Ile Phe Ser Glu Thr Lys Asp Val	
1	5

ttt caa tta aaa gac ttg gag aag att gct ccc aaa gag aaa ggc att	399
Phe Gln Leu Lys Asp Leu Glu Lys Ile Ala Pro Lys Glu Lys Gly Ile	
12 17 22 27	

act gct atg tca gta aaa gaa gtc ctt caa agc tta gtt gat gat ggt	447
Thr Ala Met Ser Val Lys Glu Val Leu Gln Ser Leu Val Asp Asp Gly	
28 33 38 43	

atg gtt gac tgt gag agg atc gga act tct aat tat tat tgg gct ttt	495
Met Val Asp Cys Glu Arg Ile Gly Thr Ser Asn Tyr Tyr Trp Ala Phe	
44 49 54 59	

cca agt aaa gct ctt cat gca agg aaa cat aag ttg gag gtt ctg gaa	543
Pro Ser Lys Ala Leu His Ala Arg Lys His Lys Leu Glu Val Leu Glu	
60 65 70 75	

tct cag ttg tct gag gga agt caa aag cat gca agc cta cag aaa agc	591
Ser Gln Leu Ser Glu Gly Ser Gln Lys His Ala Ser Leu Gln Lys Ser	
76 81 86 91	

att gag aaa gct aaa att ggc cga tgt gaa acg gaa gag cga acc agg Ile Glu Lys Ala Lys Ile Gly Arg Cys Glu Thr Glu Glu Arg Thr Arg	92 97 102 107	639
cta gca aaa gag ctt tct tca ctt cga gac caa agg gaa cag cta aag Leu Ala Lys Glu Leu Ser Ser Leu Arg Asp Gln Arg Glu Gln Leu Lys	108 113 118 123	687
gca gaa gta gaa aaa tac aaa gac tgt gat ccg caa gtt gtg gaa gaa Ala Glu Val Glu Lys Tyr Lys Asp Cys Asp Pro Gln Val Val Glu Glu	124 129 134 139	735
ata cgc caa gca aat aaa gta gcc aaa gaa gct gct aac aga tgg act Ile Arg Gln Ala Asn Lys Val Ala Lys Glu Ala Ala Asn Arg Trp Thr	140 145 150 155	783
gat aac ata ttc gca ata aaa tct tgg gcc aaa aga aaa ttt ggg ttt Asp Asn Ile Phe Ala Ile Lys Ser Trp Ala Lys Arg Lys Phe Gly Phe	156 161 166 171	831
gaa gaa aat aaa att gat aga act ttt gga att cca gaa gac ttt gac Glu Glu Asn Lys Ile Asp Arg Thr Phe Gly Ile Pro Glu Asp Phe Asp	172 177 182 187	879
tac ata gac taa aat attccatgggt ggtgaaggat gtacaagctt gtgaatatgt Tyr Ile Asp *	188	934
aaattttaaa ctattatcta actaagtgtta ctgaattgtc gtttgctgt aactgtgttt		994
atcatttat taatgttaaa taaagtgtaa aatgcagatg ttcttcaccc ctttggtag		1054
aacaaaagca ggatgataac catatcccc cagtgcctcat caaagtagga cactaaaaat		1114
ccatccatct cagtcaaagt cgagcggccg cgaatttagt agtagtagcg gccgctctag		1174
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ttaagaaagg aattcttagca aagttattct gtaaatacaa cagaatcagt tgctttgtt	180
aaatatattg gtgcaagttc aac atg gag gca aat cac tgc tcc ctg ggt Met Glu Ala Asn His Cys Ser Leu Gly	230
1 5	
gtg tat cca tct tac cca gac ctg gtc atc gat gtc gga gaa gtg act Val Tyr Pro Ser Tyr Pro Asp Leu Val Ile Asp Val Gly Glu Val Thr	278
10 15 20 25	
ctg gga gaa gaa aac aga aaa aag cta cag aaa act cag aga gac caa Leu Gly Glu Glu Asn Arg Lys Lys Leu Gln Lys Thr Gln Arg Asp Gln	326
26 31' 36 41	
gag agg gcg aga gtt ata cgg gcc gcg tgt gct tta tta aac tca gga Glu Arg Ala Arg Val Ile Arg Ala Ala Cys Ala Leu Leu Asn Ser Gly	374
42 47 52 57	
gga gga gtg att cag atg gaa atg gcc aac agg gat gag cgt ccc aca Gly Gly Val Ile Gln Met Glu Met Ala Asn Arg Asp Glu Arg Pro Thr	422
58 63 68 73	
gag atg gga ctg gat tta gaa gaa tcc ttg aga aag ctt att cag tat Glu Met Gly Leu Asp Leu Glu Glu Ser Leu Arg Lys Leu Ile Gln Tyr	470
74 79 84 89	
cca tat ttg cag gct ttc ttt gag act aag caa cac gga agg tgt ttt Pro Tyr Leu Gln Ala Phe Phe Glu Thr Lys Gln His Gly Arg Cys Phe	518
90 95 100 105	
tat att ttt gtt aaa tct tgg agt ggt gat cct ttc ctt aaa gat ggt Tyr Ile Phe Val Lys Ser Trp Ser Gly Asp Pro Phe Leu Lys Asp Gly	566
106 111 116 121	
tct ttc aat tcc cgc att tgc agc ctt act tcg gct atc tac atg cag Ser Phe Asn Ser Arg Ile Cys Ser Leu Thr Ser Ala Ile Tyr Met Gln	614
122 127 132 137	
atg aat gag acc agg ccc tta ttt cac acc ata tac taa aatcatctca Met Asn Glu Thr Arg Pro Leu Phe His Thr Ile Tyr *	663
138 143 148	
aaatacatta taatgcagac ataagatgog aaactgtaaa actactggaa gaaaacacag	723
ggaaaaatct ccatgatact ggtctggca atgtttcct ggatatgacc ccaaatacac	783
agtccccc acgtaaatta acagatgccca ttataag	819

<210> 1094
<211> 2350
<212> DNA
<213> Homo sapiens

<220>

<221> CDS
<222> (202)..(1929)

<400> 1094

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gt	ggcgatg	cggccgttag	ccggcggggg	aggtgctgct	gctgcctcca	ctgtactcag	120
ac	ccaggtac	cacaggattt	tccatccccc	agcagctcag	tgcaacggtg	tgaactcagc	180
ct	gtttcaga	gcctccacac	c	atg acc tcc aag aag	ctg gtg aac	tcg gtg	231
				Met Thr Ser Lys Lys	Leu Val Asn Ser	Val	
		1		5			
gct	ggc	tgt	gat	gac	gct	ctt	279
Ala	Gly	Cys	Ala	Asp	Asp	Ala	
11				Leu	Ala	Gly	
					Leu	Val	
					Ala	Cys	
						Asn	Pro
				16.		21	26
aac	ctg	cag	ctc	ctg	cag	ggc	327
Asn	Leu	Gln	Leu	Leu	Gln	Gly	
27						His	
						Arg	
				32		37	42
gac	agc	ctc	aag	ggc	cgg	gtg	375
Asp	Ser	Leu	Lys	Gly	Arg	Val	
43						Ala	
						Leu	
				48		53	58
cat	gag	cct	gcc	cat	gct	ggt	423
His	Glu	Pro	Ala	His	Ala	Gly	
59						Phe	
				64		69	74
gtc	atc	gcf	gga	gct	gtg	ttc	471
Val	Ile	Ala	Gly	Ala	Val	Phe	
75						Thr	
				80		85	90
gca	gcc	atc	agg	gcc	gtg	gcc	519
Ala	Ala	Ile	Arg	Ala	Val	Ala	
91						Gln	
				96		101	106
atc	gtg	aag	aac	tac	act	ggg	567
Ile	Val	Lys	Asn	Tyr	Thr	Gly	
107						Asp	
				112		117	122
gag	cag	gcc	cgg	gct	gaa	ggc	615
Glu	Gln	Ala	Arg	Ala	Glu	Gly	
123						Ile	
				128		133	138
gac	gac	agc	gcc	ttc	act	gtc	663
Asp	Asp	Ser	Ala	Phe	Thr	Val	
139						Leu	
				144		149	154
tgc	ggc	acc	gtg	ctt	ata	cac	711
Cys	Gly	Thr	Val	Leu	Ile	His	
155						Lys	
				160		165	170
ggt	gtg	ggg	ctg	gag	gag	atc	759
Gly	Val	Gly	Leu	Glu	Glu	Ile	
171						Ala	
				176		181	186

gcc atg ggt acc ctg ggg gtg agc tta tcc tcc tgc agc gtc cct ggt		807
Ala Met Gly Thr Leu Gly Val Ser Leu Ser Ser Cys Ser Val Pro Gly		
187	192	197
202		
tcc aaa ccc acc ttc gag ctc tca gcc gac gag gtg gag ctg ggc ctg		855
Ser Lys Pro Thr Phe Glu Leu Ser Ala Asp Glu Val Glu Leu Gly Leu		
203	208	213
218		
ggg atc cac ggg gaa gct ggt gtg cgc cgg ata aag atg gca acc gcc		903
Gly Ile His Gly Glu Ala Gly Val Arg Arg Ile Lys Met Ala Thr Ala		
219	224	229
234		
gat gag att gtg aaa ctc atg ctc gac cac atg aca aac acc acc aac		951
Asp Glu Ile Val Lys Leu Met Leu Asp His Met Thr Asn Thr Thr Asn		
235	240	245
250		
gcg tcc cat gtg cct gtg cag ccc ggc tcc tca gtt gtg atg atg gtc		999
Ala Ser His Val Pro Val Gln Pro Gly Ser Ser Val Val Met Met Val		
251	256	261
266		
aac aac ctg ggt ggc ctg tca ttc ctg gaa ctg ggc atc ata gcc gac		1047
Asn Asn Leu Gly Gly Leu Ser Phe Leu Glu Leu Gly Ile Ile Ala Asp		
267	272	277
282		
gct acc gtc cgc tcc ctg gag ggc cgc ggg gtg aag att gcc cgt gcc		1095
Ala Thr Val Arg Ser Leu Glu Gly Arg Gly Val Lys Ile Ala Arg Ala		
283	288	293
298		
ctg gtg ggc acc ttc atg tca gca ctg gag atg cct ggc att tct ctc		1143
Leu Val Gly Thr Phe Met Ser Ala Leu Glu Met Pro Gly Ile Ser Leu		
299	304	309
314		
acc ctc ctg ctg gtg gat gag cct ctc ctg aaa ctg ata gat gct gaa		1191
Thr Leu Leu Val Asp Glu Pro Leu Leu Lys Leu Ile Asp Ala Glu		
315	320	325
330		
acc act gca gca gcc tgg cct aac gtg gct gca gtc tcc att act ggg		1239
Thr Thr Ala Ala Ala Trp Pro Asn Val Ala Ala Val Ser Ile Thr Gly		
331	336	341
346		
cgg aag cgg agc cgg gta gcc cct gcc gag ccc cag gag gcc cct gat		1287
Arg Lys Arg Ser Arg Val Ala Pro Ala Glu Pro Gln Glu Ala Pro Asp		
347	352	357
362		
tcc act gct gca gga ggc tca gcc tcg aag cgg atg gcg ctg gtg ctg		1335
Ser Thr Ala Ala Gly Gly Ser Ala Ser Lys Arg Met Ala Leu Val Leu		
363	368	373
378		
gaa cgg gtg tgc agc act ctc ctg ggc ctg gag gaa cac ctg aat gcc		1383
Glu Arg Val Cys Ser Thr Leu Leu Gly Leu Glu Glu His Leu Asn Ala		
379	384	389
394		
/ ctg gac cgg gct gct ggt gac ggc gac tgt ggc acc acc cac agc cgt		1431
Leu Asp Arg Ala Ala Gly Asp Gly Asp Cys Gly Thr Thr His Ser Arg		
395	400	405
410		

gcg gcc aga gca atc cag gag tgg ctg aag gag ggc cca ccc cct gcc Ala Ala Arg Ala Ile Gln Glu Trp Leu Lys Glu Gly Pro Pro Pro Ala 411 416 421 426	1479
agc cct gcc cag ctg ctc tcc aag ttg tct gtt ctg ctc ctg gag aag Ser Pro Ala Gln Leu Leu Ser Lys Leu Ser Val Leu Leu Glu Lys 427 432 437 442	1527
atg gga ggc tca tct ggg gcg ctc tat ggc ctg ttc ctg act gcg gct Met Gly Gly Ser Ser Gly Ala Leu Tyr Gly Leu Phe Leu Thr Ala Ala 443 448 453 458	1575
gca cag ccc ctg aag gcc aag acc agc ctc cca gcc tgg tct gct gcc Ala Gln Pro Leu Lys Ala Lys Thr Ser Leu Pro Ala Trp Ser Ala Ala 459 464 469 474	1623
atg gat gcc ggc ctg gaa gcc atg cag aag tat ggc aag gct gct cca Met Asp Ala Gly Leu Glu Ala Met Gln Lys Tyr Gly Lys Ala Ala Pro 475 480 485 490	1671
ggg gac agg act atg ctg gat tct ctg tgg gca gcg ggg cag gag ctc Gly Asp Arg Thr Met Leu Asp Ser Leu Trp Ala Ala Gly Gln Glu Leu 491 496 501 506	1719
caa gcc tgg aag agc cca gga gct gat ctg tta caa gtc ctg acc aaa Gln Ala Trp Lys Ser Pro Gly Ala Asp Leu Leu Gln Val Leu Thr Lys 507 512 517 522	1767
gca gtc aag agt gcc gaa gct gca gcc gag gcc acc aag aat atg gaa Ala Val Lys Ser Ala Glu Ala Ala Glu Ala Thr Lys Asn Met Glu 523 528 533 538	1815
gct gga gcc gga aga gcc agt tat atc agc tca gca cggtt ctg gag cag Ala Gly Ala Gly Arg Ala Ser Tyr Ile Ser Ala Arg Leu Glu Gln 539 544 549 554	1863
cca gac ccc ggg gcg gtg gca gct gct gcc atc ctc cggtt gcc atc ttg Pro Asp Pro Gly Ala Val Ala Ala Ala Ile Leu Arg Ala Ile Leu 555 560 565 570	1911
gag gtc ttg cag agc tag ggtgtg tgactgcctc ccttggcctc agtcctctc Glu Val Leu Gln Ser *	1965
571 576	
actgctgtgc tgagggtggcc ttgtcactt ctttgcctt tccaaaccctc accttcccccc	2025
ggcctggccc cattggccca ccctctaagt tgagcaggaa atccctccacc aagttccag	2085
aactacagac agcacccaga gtgagctgga gtgggtcccc atgcctctcc agcatgccct	2145
ttcccttgc aggagggtgg agtccctggg tcatgcctc ccctgccagc tctgggttc	2205
agagataagg catttcctt gtgcagcctt tacctggcaa tcctaatttg gtttaagac	2265
tccctgtcaa atgctttccg caccttaacc ccagtgagcg tgaaaaagaa agttaataaa	2325
ctataataca tggaaaaaaaaaaaaa	2350

<210> 1095
<211> 1200
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (118)..(708)

<400> 1095

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ggagccgaag	cgcgcaggcc	cgtcccggtg	gccggggagc	gggcgggtgg	gggcgcc	117
atg tgg ttc atg tac ctg ctg agc tgg ctg tcg ctc ttc atc cag gtg						165
Met Trp Phe Met Tyr Leu Leu Ser Trp Leu Ser Leu Phe Ile Gln Val						
1	5	10		15		
gcc ttc atc acg ctg gct gtc gcg gct gga ctc tat tac ctg gca gaa						213
Ala Phe Ile Thr Leu Ala Val Ala Ala Gly Leu Tyr Tyr Leu Ala Glu						
17	22	27		32		
ctg ata gaa gaa tac aca gtg gcc acc agc agg atc ata aaa tac atg						261
Leu Ile Glu Glu Tyr Thr Val Ala Thr Ser Arg Ile Ile Lys Tyr Met						
33	38	43		48		
atc tgg ttc tcc acc gct gta ctg att ggc ctc tac gtc ttt gag cgc						309
Ile Trp Phe Ser Thr Ala Val Leu Ile Gly Leu Tyr Val Phe Glu Arg						
49	54	59		64		
ttc ccc acc agc atg att gga gtg ggc cta ttc acc aac ctc gtc tac						357
Phe Pro Thr Ser Met Ile Gly Val Gly Leu Phe Thr Asn Leu Val Tyr						
65	70	75		80		
ttt ggc ctc ctc cag acc ttc ccc ttc atc atg ctg acc tcg cct aac						405
Phe Gly Leu Leu Gln Thr Phe Pro Phe Ile Met Leu Thr Ser Pro Asn						
81	86	91		96		
ttc atc ctg tcg tgt gga cta gtg gtg aat cat tac cta gca ttt						453
Phe Ile Leu Ser Cys Gly Leu Val Val Val Asn His Tyr Leu Ala Phe						
97	102	107		112		
cag ttt ttt gca gaa gaa tat tat ccc ttc tca gag gtc ctg gcc tat						501
Gln Phe Phe Ala Glu Glu Tyr Tyr Pro Phe Ser Glu Val Leu Ala Tyr						
113	118	123		128		
ttc act ttc tgc ctg tgg ata att ccg ttt gcg ttt ttt gtg tca ctt						549
Phe Thr Phe Cys Leu Trp Ile Ile Pro Phe Ala Phe Phe Val Ser Leu						
129	134	139		144		
tcg gcc ggg gag aac gtc ctg ccc tct acc atg cag cca gga gat gat						597
Ser Ala Gly Glu Asn Val Leu Pro Ser Thr Met Gln Pro Gly Asp Asp						
145	150	155		160		

gtc gtc tcc aat tat ttc acc aaa ggc aag cgg ggc aaa cgc tta ggg		645
Val Val Ser Asn Tyr Phe Thr Lys Gly Lys Arg Gly Lys Arg Leu Gly		
161	166	171
		176
atc ctg gtt gtc ttc tcc atc aaa gag gcc att cta ccc agt cgt		693
Ile Leu Val Val Phe Ser Phe Ile Lys Glu Ala Ile Leu Pro Ser Arg		
177	182	187
		192
cag aag ata tac tga cccccatgca ggcaggatgt ggggggcaag atcaggagag		748
Gln Lys Ile Tyr *		
193		
tcaggcccct gggcctctat gccaggtggg gaccagaagt cgggaaggca cctaccacct		808
gccctggctt tcctccccc aactctggag ccccatcccc accctccttg gggggctcag		868
cttggctcag atctgatgct tcaagaggct gtaacctcag agggcaccaa ggagggtggc		928
agagcctgtt tagccaggag gccgaggtcc ctcagtcctc ccctgtccct tccaaggtgg		988
gtcaggaggt tctggccccc ctggggcagg cagggcaggg tctgtgaagc ttaagagcag		1048
atggtgacaa gttctctggg caggtggcca tggggagggg ccatggcttg gcatgtccaa		1108
cagaaatagt ttttgcgttt gaacgggtgat ttctgtccaa gtgcagattt ccgtttgaat		1168
aaagcttcgc taataggtgg aaaaaaaaaaa aa		1200

<210> 1096
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 <212> DNA
 <213> Homo sapiens

<220>
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 <222> (71)..(1495)

<400> 1096

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cggcgccgggt atg gag ctt ggg ggt cac tgg gac atg aac tcg gcc ccg		109
Met Glu Leu Gly Gly His Trp Asp Met Asn Ser Ala Pro		
1	5	10
agg ctg gtc tcg gag acc gca gag cgg aaa cag gag cag aag aca gga		157
Arg Leu Val Ser Glu Thr Ala Glu Arg Lys Gln Glu Gln Lys Thr Gly		
14	19	24
		29
acc gag gcg gag gct gcc gac tcc ggt gcc gtc gga gcc cgc cgc ttc		205
Thr Glu Ala Glu Ala Ala Asp Ser Gly Ala Val Gly Ala Arg Arg Phe		
30	35	40
		45
ctg ctc tgt ctc tac ttg ggg ggc ttc ttg gat ttg ttt ggt gtc agc		253
Leu Leu Cys Leu Tyr Leu Gly Gly Phe Leu Asp Leu Phe Gly Val Ser		

46	51	56	61	
atg gtt gtg cct tta ttg agc ctt cat gtc aag tcc ctt gga gca agt Met Val Val Pro Leu Leu Ser Leu His Val Lys Ser Leu Gly Ala Ser				301
62	67	72	77	
cca aca gtt gct gga ata gta ggc tcc tcc tat ggc att ttg caa ctc Pro Thr Val Ala Gly Ile Val Gly Ser Ser Tyr Gly Ile Leu Gln Leu				349
78	83	88	93	
ttt tct agc aca ttg gtg ggc tgc tgg agc gat gta gtg gga aga cgg Phe Ser Ser Thr Leu Val Gly Cys Trp Ser Asp Val Val Gly Arg Arg				397
94	99	104	109	
tct tcc ttg ctg gca tgc att cta ctc agt gct ctg ggc tat ctc ctt Ser Ser Leu Leu Ala Cys Ile Leu Leu Ser Ala Leu Gly Tyr Leu Leu				445
110	115	120	125	
ctc gga gca gcc acc aat gtg ttt ctg ttt gtc ctg gct aga gtc ccg Leu Gly Ala Ala Thr Asn Val Phe Leu Phe Val Leu Ala Arg Val Pro				493
126	131	136	141	
gca ggt att ttt aaa cac act ctc tcc atc tca agg gct cta ctt tct Ala Gly Ile Phe Lys His Thr Leu Ser Ile Ser Arg Ala Leu Leu Ser				541
142	147	152	157	
gat gtg gtt cca gag aag gaa cggtt gtc atc gga cac ttc aac Asp Val Val Pro Glu Lys Glu Arg Pro Leu Val Ile Gly His Phe Asn				589
158	163	168	173	
aca gcc tcc ggt gtg ggc ttc atc ttg ggc ccc gtg gtc ggt ggc tat Thr Ala Ser Gly Val Gly Phe Ile Leu Gly Pro Val Val Gly Gly Tyr				637
174	179	184	189	
ctc act gaa tta gag gat ggg ttt tat ctc aca gcc ttc atc tgc ttt Leu Thr Glu Leu Glu Asp Gly Phe Tyr Leu Thr Ala Phe Ile Cys Phe				685
190	195	200	205	
ttg gtc ttc att ctc aat gct ggt ctc gtt tgg ttc ttt cca tgg agg Leu Val Phe Ile Leu Asn Ala Gly Leu Val Trp Phe Phe Pro Trp Arg				733
206	211	216	221	
gaa gca aaa ccg ggc agt aca gag aag ggc ctg cca ttg cga aag acc Glu Ala Lys Pro Gly Ser Thr Glu Lys Gly Leu Pro Leu Arg Lys Thr				781
222	227	232	237	
cat gtg ctg ttg gga agg agc cat gac aca gtg cag gag gca gcc acc His Val Leu Leu Gly Arg Ser His Asp Thr Val Gln Glu Ala Ala Thr				829
238	243	248	253	
agc cgc aga gcc agg gcc agc aag aag act gcc cag ccc tgg gtc gaa Ser Arg Arg Ala Arg Ala Ser Lys Lys Thr Ala Gln Pro Trp Val Glu				877
254	259	264	269	
gta gtg ttg gcc ttg cgg aac atg aag aac ctg ctg ttt tcc gaa atg Val Val Leu Ala Leu Arg Asn Met Lys Asn Leu Leu Phe Ser Glu Met				925
270	275	280	285	

tgg gac ata ttt ctg gtg cgc ttg ctg atg gcc atg gca gtc atg ctg Trp Asp Ile Phe Leu Val Arg Leu Leu Met Ala Met Ala Val Met Leu	973
286 291 296 301	
tac tac agt aac ttt gtc ctg gcc ctg gag gag cgc ttt ggg gtg cgg Tyr Tyr Ser Asn Phe Val Leu Ala Leu Glu Glu Arg Phe Gly Val Arg	1021
302 307 312 317	
ccc aag gtg aca ggc tac ctc atc agt tac agc agc atg ctg ggg gcc Pro Lys Val Thr Gly Tyr Leu Ile Ser Tyr Ser Ser Met Leu Gly Ala	1069
318 323 328 333	
gtg gcc ggc ctt gcc ctg ggg cca atc cta cggt tac aag cac aac Val Ala Gly Leu Ala Leu Gly Pro Ile Leu Arg Leu Tyr Lys His Asn	1117
334 339 344 349	
tcg cag gca ctg ctg cat tcc agc ata ctc acc tgc aca ctg ctg Ser Gln Ala Leu Leu His Ser Ser Ile Leu Thr Cys Thr Leu Leu	1165
350 355 360 365	
ctg ctc tac tcc ttg gcc ccc acc atg ggt gca gtt gtc ctc tcc tcc Leu Leu Tyr Ser Leu Ala Pro Thr Met Gly Ala Val Val Leu Ser Ser	1213
366 371 376 381	
act ctc ctg tcc ttc tcc act gcc att ggc agg acg tgc atc acg gac Thr Leu Leu Ser Phe Ser Thr Ala Ile Gly Arg Thr Cys Ile Thr Asp	1261
382 387 392 397	
ctc cag ctg act gtg ggc ggg gcc cag gcc agc ggc acc ctt att ggc Leu Gln Leu Thr Val Gly Gly Ala Gln Ala Ser Gly Thr Leu Ile Gly	1309
398 403 408 413	
gtg ggg cag tct gtg act gca gtg ggc cgc atc atc gcc cct ctc ctc Val Gly Gln Ser Val Thr Ala Val Gly Arg Ile Ile Ala Pro Leu Leu	1357
414 419 424 429	
tcg ggg gtt gcc cag qag gtc agc cct tgc ggc ccc ccc agc ctg ggc Ser Gly Val Ala Gln Glu Val Ser Pro Cys Gly Pro Pro Ser Leu Gly	1405
430 435 440 445	
gct gtg tta gcc tta gtg gcc att ttc ata atg tct cta aac aag cga Ala Val Leu Ala Leu Val Ala Ile Phe Ile Met Ser Leu Asn Lys Arg	1453
446 451 456 461	
cac tct agt ggt gat ggg aat agt aaa tta aaa agt gag tag atggatt His Ser Ser Gly Asp Gly Asn Ser Lys Leu Lys Ser Glu *	1502
462 467 472	
tggacaacat aaagcaacaa aatttgagat gggtgaatga gggccggagg ccatgatgaa	1562
aagggcactt tggaaagggt tgggttgaa gggaaatatt tccgggtggg tgtgagctgt	1622
tgggcttcca ggtcagctct tggccatgca gccatgcctg caggatgatc agaagtcacg	1682
gcacctcatg ggaaggtaa gactggagca aagctttcc aagtgtgacc cagagaccag	1742

tagcatcagc atcacctgag acctgtgaac actgaagctc cagctcagac atgttgggga	1802
ccatTTtaat aagataaccta gctgatttt tgcacagcaa acttgaaaa cccctggct	1862
aagggttagt atttgatca cttatggaat ataatctcg ggaaattaaa ttctgctcaa	1922
ttgaaaaaaaaaaaa	1937

<210> 1097
 <211> 3144
 <212> DNA
 <213> Homo sapiens

<220>
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 <222> (129)..(2027)

<400> 1097	
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tctgccgttg ggtgaggcgc ggagcgaagt gaagggtggc ccaggtgggg ccaggctgac	120
tgaaaaag atg gat act atg atg ctg aat gtg cgg aat ctg ttt gag cag	170
Met Asp Thr Met Met Leu Asn Val Arg Asn Leu Phe Glu Gln	
1 5 10	
ctt gtg cgc cgg gtg gag att ctc agt gaa gga aat gaa gtc caa ttt	218
Leu Val Arg Arg Val Glu Ile Leu Ser Glu Gly Asn Glu Val Gln Phe	
15 20 25 30	
atc cag ttg gcg aag gac ttt gag gat ttc cgt aaa aag tgg cag agg	266
Ile Gln Leu Ala Lys Asp Phe Glu Asp Phe Arg Lys Lys Trp Gln Arg	
31 36 41 46	
act gac cat gag ctg ggg aaa tac aag gat ctt ttg atg aaa gca gag	314
Thr Asp His Glu Leu Gly Lys Tyr Lys Asp Leu Leu Met Lys Ala Glu	
47 52 57 62	
act gag cga agt gct ctg gat gtt aag ctg aag cat gca cgt aat cag	362
Thr Glu Arg Ser Ala Leu Asp Val Lys Leu Lys His Ala Arg Asn Gln	
63 68 73 78	
gtg gat gta gag atc aaa cgg aga cag aga gct gag gct gac tgc gaa	410
Val Asp Val Glu Ile Lys Arg Arg Gln Arg Ala Glu Ala Asp Cys Glu	
79 84 89 94	
aag ctg gaa cga cag att cag ctg att cga gag atg ctc atg tgt gac	458
Lys Leu Glu Arg Gln Ile Gln Leu Ile Arg Glu Met Leu Met Cys Asp	
95 100 105 110	
aca tct ggc agc att caa cta agc gag gag caa aaa tca gct ctg gct	506
Thr Ser Gly Ser Ile Gln Leu Ser Glu Glu Gln Lys Ser Ala Leu Ala	
111 116 121 126	

ttt ctc aac aga ggc caa cca tcc agc agc aat gct ggg aac aaa aga		554	
Phe Leu Asn Arg Gly Gln Pro Ser Ser Ser Asn Ala Gly Asn Lys Arg			
127	132	137	142
cta tca acc att gat gaa tct ggt tcc att tta tca gat atc agc ttt		602	
Leu Ser Thr Ile Asp Glu Ser Gly Ser Ile Leu Ser Asp Ile Ser Phe			
143	148	153	158
gac aag act gat gaa tca ctg gat tgg gac tct tct ttg gtg aag act		650	
Asp Lys Thr Asp Glu Ser Leu Asp Trp Asp Ser Ser Leu Val Lys Thr			
159	164	169	174
ttc aaa ctg aag aag aga gaa aag agg cgc tct act agc cga cag ttt		698	
Phe Lys Leu Lys Lys Arg Glu Lys Arg Arg Ser Thr Ser Arg Gln Phe			
175	180	185	190
gtt gat ggt ccc cct gga cct gta aag aaa act cgt tcc att ggc tct		746	
Val Asp Gly Pro Pro Gly Pro Val Lys Lys Thr Arg Ser Ile Gly Ser			
191	196	201	206
gca gta gac cag ggg aat gaa tcc ata gtt gca aaa act aca gtg act		794	
Ala Val Asp Gln Gly Asn Glu Ser Ile Val Ala Lys Thr Thr Val Thr			
207	212	217	222
gtt ccc aat gat ggc ggg ccc atc gaa gct gtg tcc act att gag act		842	
Val Pro Asn Asp Gly Gly Pro Ile Glu Ala Val Ser Thr Ile Glu Thr			
223	228	233	238
gtg cca tat tgg acc agg agc cga agg aaa aca ggt act tta caa cct		890	
Val Pro Tyr Trp Thr Arg Ser Arg Arg Lys Thr Gly Thr Leu Gln Pro			
239	244	249	254
tgg aac agt gac tcc acc ctg aac agc agg cag ctg gag cca aga act		938	
Trp Asn Ser Asp Ser Thr Leu Asn Ser Arg Gln Leu Glu Pro Arg Thr			
255	260	265	270
gag aca gac agt gtg ggc acg cca cag agt aat gga ggg atg cgc ctg		986	
Glu Thr Asp Ser Val Gly Thr Pro Gln Ser Asn Gly Gly Met Arg Leu			
271	276	281	286
cat gac ttt gtt tct aag acg gtt att aaa cct gaa tcc tgt gtt cca		1034	
His Asp Phe Val Ser Lys Thr Val Ile Lys Pro Glu Ser Cys Val Pro			
287	292	297	302
tgt gga aag cgg ata aaa ttt ggc aaa tta tct ctg aag tgt cga gac		1082	
Cys Gly Lys Arg Ile Lys Phe Gly Lys Leu Ser Leu Lys Cys Arg Asp			
303	308	313	318
tgt cgt gtg gtc tct cat cca gaa tgt cgg gac cgc tgt ccc ctt ccc		1130	
Cys Arg Val Val Ser His Pro Glu Cys Arg Asp Arg Cys Pro Leu Pro			
319	324	329	334
tgc att cct acc ctg ata gga aca cct gtc aag att gga gag gga atg		1178	
Cys Ile Pro Thr Leu Ile Gly Thr Pro Val Lys Ile Gly Glu Gly Met			
335	340	345	350
ctg gca gac ttt gtg tcc cag act tct cca atg atc ccc tcc att gtt		1226	

Leu Ala Asp Phe Val Ser Gln Thr Ser Pro Met Ile Pro Ser Ile Val			
351	356	361	366
gtg cat tgt gta aat gag att gag caa aga ggt ctg act gag aca ggc			1274
Val His Cys Val Asn Glu Ile Glu Gln Arg Gly Leu Thr Glu Thr Gly			
367	372	377	382
ctg tat agg atc tct ggc tgt gac cgc aca gta aaa gag ctg aaa gag			1322
Leu Tyr Arg Ile Ser Gly Cys Asp Arg Thr Val Lys Glu Leu Lys Glu			
383	388	393	398
aaa ttc ctc aga gtg aaa act gta ccc ctc ctc agc aaa gtg gat gat			1370
Lys Phe Leu Arg Val Lys Thr Val Pro Leu Leu Ser Lys Val Asp Asp			
399	404	409	414
atc cat gct atc tgt agc ctt cta aaa gac ttt ctt cga aac ctc aaa			1418
Ile His Ala Ile Cys Ser Leu Leu Lys Asp Phe Leu Arg Asn Leu Lys			
415	420	425	430
gaa cct ctt ctg acc ttt cgc ctt aac aga gcc ttt atg gaa gca gca			1466
Glu Pro Leu Leu Thr Phe Arg Leu Asn Arg Ala Phe Met Glu Ala Ala			
431	436	441	446
gaa atc aca gat gaa gac aac agc ata gct gcc atg tac caa gct gtt			1514
Glu Ile Thr Asp Glu Asp Asn Ser Ile Ala Ala Met Tyr Gln Ala Val			
447	452	457	462
ggt gaa ctg ccc cag gcc aac agg gac aca tta gct ttc ctc atg att			1562
Gly Glu Leu Pro Gln Ala Asn Arg Asp Thr Leu Ala Phe Leu Met Ile			
463	468	473	478
cac ttg cag aga gtg gct cag agt cca cat act aaa atg gat gtt gcc			1610
His Leu Gln Arg Val Ala Gln Ser Pro His Thr Lys Met Asp Val Ala			
479	484	489	494
aat ctg gct aaa gtc ttt ggc cct aca ata gtg gcc cat gct gtg ccc			1658
Asn Leu Ala Lys Val Phe Gly Pro Thr Ile Val Ala His Ala Val Pro			
495	500	505	510
aat cca gac cca gtg aca atg tta cag gac atc aag cgt caa ccc aag			1706
Asn Pro Asp Pro Val Thr Met Leu Gln Asp Ile Lys Arg Gln Pro Lys			
511	516	521	526
gtg gtt gag cgc ctg ctt tcc ttg cct ctg gag tat tgg agt cag ttc			1754
Val Val Glu Arg Leu Leu Ser Leu Pro Leu Glu Tyr Trp Ser Gln Phe			
527	532	537	542
atg atg gtg gag caa gag aac att gac ccc cta cat gtc att gaa aac			1802
Met Met Val Glu Gln Glu Asn Ile Asp Pro Leu His Val Ile Glu Asn			
543	548	553	558
tca aat gcc ttt tca aca cca cag aca cca gat att aaa gtg agt tta			1850
Ser Asn Ala Phe Ser Thr Pro Gln Thr Pro Asp Ile Lys Val Ser Leu			
559	564	569	574
ctg gga cct gtg acc act cct gaa cat cag ctt ctc aag act cct tca			1898
Leu Gly Pro Val Thr Thr Pro Glu His Gln Leu Leu Lys Thr Pro Ser			

575	580	585	590													
tct	ggt	tcc	ctg	tca	cag	aga	gtc	cgt	tcc	acc	ctc	acc	aag	aac	act	1946
Ser	Gly	Ser	Leu	Ser	Gln	Arg	Val	Arg	Ser	Thr	Leu	Thr	Lys	Asn	Thr	
591																
cct	aga	ttt	ggg	agc	aaa	agc	aag	tct	gcc	act	aac	cta	gga	cga	caa	1994
Pro	Arg	Phe	Gly	Ser	Lys	Ser	Lys	Ser	Ala	Thr	Asn	Leu	Gly	Arg	Gln	
607																
ggc	aac	ttt	ttt	gct	tct	cca	atg	ctc	aag	tga	agtcacat	ctgcctgtta			2045	
Gly	Asn	Phe	Phe	Ala	Ser	Pro	Met	Leu	Lys	*						
623																
ctccccagca	ttgactgact	ataagaaagg	acacatctgt	actctgtct	gcagcctcct											2105
gtactcatta	ctacttttag	cattctccag	gctttactc	aagtttaatt	gtgcatgagg											2165
gttttattaa	aactatatat	atctccccctt	ccttctcctc	aagtcacata	atatcagcac											2225
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caatgacaga	aaccctacct	atctgataag	attagctgt	ctcagggtgg	gaagtggag											2465
ggcaggggcaa	agaaaggatt	agaccagagg	attaggatg	cctccttcta	agaaccagaa											2525
gttctcattc	cccattatga	actgagctat	aatatggagc	tttcataaaaa	atggatgca											2585
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tgccgctggc	tgaactttgg	gttcattttgg	ggtcaaagcc	agttttctt	ttaaaattga											2765
attcattctg	atgctggcc	cccatcccc	caaccttgc	cagtggagcc	caacttctaa											2825
aggtcaatat	atcatcctt	ggcatccaa	ctaacaataa	agagtaggct	ataaggaaag											2885
attgtcaata	ttttgtggta	agaaaagcta	cagtcatttt	ttctttgcac	tttggatgct											2945
gaaatttttc	ccatgaaaca	tagccacatc	tagatagatg	tgagctttt	cttctgttaa											3005
aattattctt	aatgtctgta	aaaacgattt	tcttctgttag	aatgtttgac	ttcgtattga											3065
cccttatctg	taaaacacct	atttggata	atattggaa	aaaaagtaaa	tagcttttc											3125
aaagtgc当地	aaaaaaaaaa															3144

<210> 1098
<211> 2307

<212> DNA
<213> Homo sapiens

<220>
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<222> (177)..(1775)

<400> 1098

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cgccctcggtt	cctttgcaa	tttccgtcgg	gccccagccg	ccatttctc	ggcgcttgtg	120
tggctcgctg	gctgcgtggc	tcgggtcttg	tgaggcaagc	tttgcgtccgt	tcggca	176
atg	gac	gga	atc	gtc	act	176
Met	Asp	Gly	Ile	Val	Thr	176
1	5	10	15			
gac	gaa	cta	ctc	tca	ggc	176
Asp	Glu	Leu	Leu	Ser	Gly	176
17	22	27	32			
agc	agc	atg	gta	gtt	aca	176
Ser	Ser	Met	Val	Val	Thr	176
33	38	43	48			
gga	gaa	gat	aaa	atg	gat	176
Gly	Glu	Asp	Lys	Met	Asp	176
49	54	59	64			
aaa	tta	cct	ggg	gaa	gta	176
Lys	Leu	Pro	Gly	Glu	Val	176
65	70	75	80			
cct	ttt	ggt	aag	gtg	acc	176
Pro	Phe	Gly	Lys	Val	Thr	176
81	86	91	96			
gca	ttt	ttg	gaa	cta	gca	176
Ala	Phe	Leu	Glu	Leu	Ala	176
97	102	107	112			
tac	tat	tct	gtg	aca	cct	176
Tyr	Tyr	Ser	Ala	Val	Thr	176
113	118	123	128			
cag	tac	tcg	aat	cac	aaa	176
Gln	Tyr	Ser	Asn	His	Lys	176
129	134	139	144			
cgt	gct	cag	gca	gtt	ctt	176
Arg	Ala	Gln	Ala	Val	Leu	176
145	150	155	160			
act	cct	ctt	agt	ggc	acc	176
Thr	Pro	Leu	Ser	Gly	Thr	176
161	166	171	176			

cag agt cca gta ctt aga ata att att gac aac atg tac tac cct gta Gln Ser Pro Val Leu Arg Ile Ile Ile Asp Asn Met Tyr Tyr Pro Val	752
177 182 187 192	
aca ctt gat gtt ctt cac caa ata ttt tct aag ttt ggt gct gta ttg Thr Leu Asp Val Leu His Gln Ile Phe Ser Lys Phe Gly Ala Val Leu	800
193 198 203 208	
aag ata atc aca ttt aca aaa aat aac cag ttt caa gct ttg ctc cag Lys Ile Ile Thr Phe Thr Lys Asn Asn Gln Phe Gln Ala Leu Leu Gln	848
209 214 219 224	
tat ggt gat cca gta aat gct caa caa gca aaa cta gcc cta gat ggt Tyr Gly Asp Pro Val Asn Ala Gln Ala Lys Leu Ala Leu Asp Gly	896
225 230 235 240	
cag aat att tat aat gcc tgc tgt acc cta agg att gat ttt tcc aaa Gln Asn Ile Tyr Asn Ala Cys Cys Thr Leu Arg Ile Asp Phe Ser Lys	944
241 246 251 256	
ctt gtg aat ttg aat gta aaa tac aac aat gat aaa agt agg gat tat Leu Val Asn Leu Asn Val Lys Tyr Asn Asn Asp Lys Ser Arg Asp Tyr	992
257 262 267 272	
act cga cct gat ctt cca tct ggg gat gga caa cct gca ttg gac cca Thr Arg Pro Asp Leu Pro Ser Gly Asp Gly Gln Pro Ala Leu Asp Pro	1040
273 278 283 288	
gct att gct gca gca ttt gcc aag gag aca tcc ctc tta gct gtt cca Ala Ile Ala Ala Ala Phe Ala Lys Glu Thr Ser Leu Leu Ala Val Pro	1088
289 294 299 304	
gga gct ctg agt cct ttg gcc att cca aat gct gct gca gca gct gct Gly Ala Leu Ser Pro Leu Ala Ile Pro Asn Ala Ala Ala Ala Ala Ala	1136
305 310 315 320	
gca gct gct ggc cga gtg ggt atg cct gga gtc tca gct ggt ggc Ala Ala Ala Ala Gly Arg Val Gly Met Pro Gly Val Ser Ala Gly Gly	1184
321 326 331 336	
aat aca gtc ctg ttg gtt agc aat tta aat gaa gag atg gtt acg ccc Asn Thr Val Leu Leu Val Ser Asn Leu Asn Glu Glu Met Val Thr Pro	1232
337 342 347 352	
caa agt ctg ttt acc ctc ttc ggt gtt tat gga gat gtg cag cgt gtg Gln Ser Leu Phe Thr Leu Phe Gly Val Tyr Gly Asp Val Gln Arg Val	1280
353 358 363 368	
aag att tta tac aat aag aaa gac agc gct cta ata cag atg gct gat Lys Ile Leu Tyr Asn Lys Lys Asp Ser Ala Leu Ile Gln Met Ala Asp	1328
369 374 379 384	
gga aac caa tca caa ctt gcc atg aat cat ctt aat gga cag aaa atg Gly Asn Gln Ser Gln Leu Ala Met Asn His Leu Asn Gly Gln Lys Met	1376
385 390 395 400	
tat gga aaa att att cgt gtt act ctg tct aaa cat cag act gta cag	1424

Tyr	Gly	Lys	Ile	Ile	Arg	Val	Thr	Leu	Ser	Lys	His	Gln	Thr	Val	Gln	
401					406					411				416		
ctc	cct	cga	gag	gga	ctt	gat	gat	caa	ggg	cta	aca	aaa	gat	ttt	ggg	1472
Leu	Pro	Arg	Glu	Gly	Leu	Asp	Asp	Gln	Gly	Leu	Thr	Lys	Asp	Phe	Gly	
417					422					427				432		
aat	tcc	cca	ttg	cat	cgt	ttt	aag	aaa	cct	gga	tcc	aaa	aat	ttt	caa	1520
Asn	Ser	Pro	Leu	His	Arg	Phe	Lys	Lys	Pro	Gly	Ser	Lys	Asn	Phe	Gln	
433					438					443				448		
aac	att	ttt	cct	cct	tct	gcc	acc	ctt	cac	cta	tct	aat	atc	cct	cca	1568
Asn	Ile	Phe	Pro	Pro	Ser	Ala	Thr	Leu	His	Leu	Ser	Asn	Ile	Pro	Pro	
449					454					459				464		
tca	gta	gca	gaa	gag	gat	cta	cga	aca	ctg	ttc	gct	aac	act	ggg	ggc	1616
Ser	Val	Ala	Glu	Glu	Asp	Leu	Arg	Thr	Leu	Phe	Ala	Asn	Thr	Gly	Gly	
465					470					475				480		
act	gtg	aaa	gca	ttt	aag	ttt	ttt	caa	aga	gat	cac	aaa	atg	gct	ctt	1664
Thr	Val	Lys	Ala	Phe	Lys	Phe	Phe	Gln	Arg	Asp	His	Lys	Met	Ala	Leu	
481					486					491				496		
ctt	cag	atg	gca	aca	gtg	gaa	gaa	gct	att	cag	gcc	ttg	att	gat	ctt	1712
Leu	Gln	Met	Ala	Thr	Val	Glu	Glu	Ala	Ile	Gln	Ala	Leu	Ile	Asp	Leu	
497					502					507				512		
cat	aat	tat	aac	ctt	gga	gaa	aac	cat	cat	ctg	aga	gtg	tct	ttc	tcc	1760
His	Asn	Tyr	Asn	Leu	Gly	Glu	Asn	His	His	Leu	Arg	Val	Ser	Phe	Ser	
513					518					523				528		
aag	tca	aca	att	taa	aaatggaaag	atgaagattt	gggggtgaatc	acattgttca								1815
Lys	Ser	Thr	Ile	*												
529																
atgtcatcac	ctatttgact	gttcagaaaa	gtggggacca	gagtttgatt	ttttttgttt											1875
ttgttttttt	ggggtttctt	tttttttcc	atgctgttat	cattccttgg	ttataaaaatg											1935
aaatggcata	tgtaaaggca	gagttgttaa	ctgctatatt	tcatctgttc	tatagggaag											1995
ccattttgtc	tgtttaaaat	ttcagtttaa	tttgctttt	ttttttttt	ttttccttctt											2055
caacttagtt	gacatacgtg	cctaaaaaag	gaaaactagt	gttgctattt	tgcatttacg											2115
ggaaaaaaagg	attgggttgtt	tagggcaca	ctgttatatg	gggttattaaa	aatgtttaag											2175
gcaggggttt	ataaaaaaag	gttaagtttt	tttttaccac	tgttttaggga	ccttaatttt											2235
gaaatactgg	gcttttcaac	ctttttcca	aattaaacca	aaaagggtac	caggatattt											2295
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<212> DNA
<213> Homo sapiens

<220>
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<222> (40)..(1284)

<400> 1099

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				1	
gag	gtg	gag	gtg	atc agc	102
Glu	Val	Glu	Val	Ile Ser Arg His	
6	11	16	21	Leu Pro Ala Leu Gly	
Arg	Gly	Lys	Gly	Leu Arg Asn	
22	27	32	37	Cys Gln Gln Thr Ser	
agg	agt	cag	ccg	gtc	198
Arg	Ser	Gln	Pro	Pro Val	
38	43	48	53	Arg Ala Phe Leu Ile Ser Thr Leu Lys	
gac	aag	cgc	ggg	acc	246
Asp	Lys	Arg	Gly	Thr Arg Tyr Glu Leu Arg	
54	59	64	69	Glu Asn Ile Glu Gln Phe	
ttc	acc	aaa	ttt	gta	294
Phe	Thr	Lys	Phe	Val Asp Glu	
70	75	80	85	Gly Lys Ala Thr Val Arg Leu Lys Glu	
cct	cct	gtg	gat	atc	342
Pro	Pro	Val	Asp	Ile Cys	
86	91	96	101	Leu Ser Lys Ala Ile Ser Ser Ser Leu Lys	
ggt	ttc	ctt	tca	gct	390
Gly	Phe	Leu	Ser	Ala Met Arg Leu Ala His	
102	107	112	117	Arg Gly Cys Asn Val Asp	
aca	cca	gtt	tca	acg	438
Thr	Pro	Val	Ser	Thr Leu Thr Pro Val Lys	
118	123	128	133	Thr Ser Glu Phe Glu Asn	
ttt	aaa	act	aaa	atg	486
Phe	Lys	Thr	Lys	Met Val Ile Thr Ser Lys	
134	139	144	149	Lys Asp Tyr Pro Leu Ser	
aag	aat	ttt	cca	tat	534
Lys	Asn	Phe	Pro	Tyr Ser Leu Glu His	
150	155	160	165	Leu Gln Thr Ser Tyr Cys Gly	
ctt	gtc	cga	gtt	gat	582
Leu	Val	Arg	Val	Asp Met Arg Met	
166	171	176	181	Leu Cys Leu Lys Ser Leu Arg Lys	

tta gac ttg agt cac aac cat ata aaa aag ctt cca gct aca att gga		630
Leu Asp Leu Ser His Asn His Ile Lys Lys Leu Pro Ala Thr Ile Gly		
182 187 192 197		
gac ctc ata cac ctt caa gaa ctt aac ctg aat gac aat cac ttg gag		678
Asp Leu Ile His Leu Gln Glu Leu Asn Leu Asn Asp Asn His Leu Glu		
198 203 208 213		
tca ttt agt gta gcc ttg tgt cat tct aca ctc cag aag tca ctt cg		726
Ser Phe Ser Val Ala Leu Cys His Ser Thr Leu Gln Lys Ser Leu Arg		
214 219 224 229		
agt ttg gac ctc agc aag aac aaa atc aag gca ctc cct gtg cag ttt		774
Ser Leu Asp Leu Ser Lys Asn Lys Ile Lys Ala Leu Pro Val Gln Phe		
230 235 240 245		
tgc cag ctc cag gaa ctt aag aat tta aaa ctt gac gat aat gaa ttg		822
Cys Gln Leu Gln Glu Leu Lys Asn Leu Lys Leu Asp Asp Asn Glu Leu		
246 251 256 261		
att caa ttt cct tgc aag ata gga caa cta ata aac ctt cgc ttt ttg		870
Ile Gln Phe Pro Cys Lys Ile Gly Gln Leu Ile Asn Leu Arg Phe Leu		
262 267 272 277		
tca gca gct cga aat aag ctt cca ttt ttg cct agt gaa ttt aga aat		918
Ser Ala Ala Arg Asn Lys Leu Pro Phe Leu Pro Ser Glu Phe Arg Asn		
278 283 288 293		
tta tcc ctt gaa tac ttg gat ctt ttt gga aat act ttt gaa caa cca		966
Leu Ser Leu Glu Tyr Leu Asp Leu Phe Gly Asn Thr Phe Glu Gln Pro		
294 299 304 309		
aaa gtc ctt cca gta ata aag ctg caa gca cca tta act tta ttg gaa		1014
Lys Val Leu Pro Val Ile Lys Leu Gln Ala Pro Leu Thr Leu Leu Glu		
310 315 320 325		
tct tct gca cga acc ata tta cat aat agg att cca tat ggc tct cat		1062
Ser Ser Ala Arg Thr Ile Leu His Asn Arg Ile Pro Tyr Gly Ser His		
326 331 336 341		
atc att cca ttc cat ctc tgc caa gat ttg gat acc gca aaa att tgt		1110
Ile Ile Pro Phe His Leu Cys Gln Asp Leu Asp Thr Ala Lys Ile Cys		
342 347 352 357		
gtt tgt gga aga ttc tgt ctg aac tct ttc att caa gga act act acc		1158
Val Cys Gly Arg Phe Cys Leu Asn Ser Phe Ile Gln Gly Thr Thr Thr		
358 363 368 373		
atg aat ctg cat tct gtt gcc cac act gtg gtc tta gta gat aat ttg		1206
Met Asn Leu His Ser Val Ala His Thr Val Val Leu Val Asp Asn Leu		
374 379 384 389		
ggg ggt act gaa gca cct att atc tct tat ttc tgt tct cta ggc tgt		1254
Gly Gly Thr Glu Ala Pro Ile Ile Ser Tyr Phe Cys Ser Leu Gly Cys		
390 395 400 405		
tat gtt aat tcc tct gat atg tta aag taa t gggtgagacc agaaaaagaa		1305

Tyr Val Asn Ser Ser Asp Met Leu Lys *
406 411

atttcaataa cagatcagtt tgggtgcat gtatgattt gcagcgtcaa attggagtaa 1365
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<222> (117)..(1229)

<400> 1100
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atg gac atg gtg cac ctg gtc cat gcc aag aat gcc cag gct ctg gcc 164
Met Asp Met Val His Leu Val His Ala Lys Asn Ala Gln Ala Leu Ala
1 5 " 10 15
agc gac cac gac tac agg aca cag tat cac aag ttc aca gca ctg ccc 212
Ser Asp His Asp Tyr Arg Thr Gln Tyr His Lys Phe Thr Ala Leu Pro
17 22 27 32
gag gac ctg aag atg gcc tgg gcc aag aaa gcc cat gcc ctg cag agt 260
Glu Asp Leu Lys Met Ala Trp Ala Lys Lys Ala His Ala Leu Gln Ser
33 38 43 48
gag ttg cgc tac aag tca gac ctg atc ggc atg aag ggc ata gga tgg 308
Glu Leu Arg Tyr Lys Ser Asp Leu Ile Gly Met Lys Gly Ile Gly Trp
49 54 59 64
ctg gcg ctg aga tcc cca cag atg gag agt gca aag aag gct gga gaa 356
Leu Ala Leu Arg Ser Pro Gln Met Glu Ser Ala Lys Lys Ala Gly Glu
65 70 75 80
ctc atc agc gag acc aag tac cgt aaa aaa cca gac agt atc aag ttc 404
Leu Ile Ser Glu Thr Lys Tyr Arg Lys Lys Pro Asp Ser Ile Lys Phe
81 86 91 96
acc aca gtg gtt gac tcc cca gac ctg gtt cat gcc aag aac agc tat 452
Thr Thr Val Val Asp Ser Pro Asp Leu Val His Ala Lys Asn Ser Tyr
97 102 107 112
atg cac tgc aat gag cgc atg tat aga tct gga gat gca gaa tcc ctg 500 /
Met His Cys Asn Glu Arg Met Tyr Arg Ser Gly Asp Ala Glu Ser Leu
113 118 123 128

cac aga tac acc ctg atc ccc gac cat ccc gat ttc acc cga gct cgc His Arg Tyr Thr Leu Ile Pro Asp His Pro Asp Phe Thr Arg Ala Arg	548
129 134 139 144	
ctc aat gcg ctg cat ctg agt gac aaa gtc tac aga aac tcc tgg gag Leu Asn Ala Leu His Leu Ser Asp Lys Val Tyr Arg Asn Ser Trp Glu	596
145 150 155 160	
cag acc cg ^g gct ggc agt tat gac ttc agg ctg gat gcc atc ccc ttc Gln Thr Arg Ala Gly Ser Tyr Asp Phe Arg Leu Asp Ala Ile Pro Phe	644
161 166 171 176	
cag act gcc cg ^g gca tct agg gag atc gcc agt gat ttc cg ^g tac aaa Gln Thr Ala Arg Ala Ser Arg Glu Ile Ala Ser Asp Phe Arg Tyr Lys	692
177 182 187 192	
gag gct ttc ctg cg ^g gac cga ggc ctg cag atc ggg tac cgc agt gtc Glu Ala Phe Leu Arg Asp Arg Gly Leu Gln Ile Gly Tyr Arg Ser Val	740
193 198 203 208	
gac gat gac cca agg atg aag cat ttc ctc aac gtt ggc agg ctc cag Asp Asp Asp Pro Arg Met Lys His Phe Leu Asn Val Gly Arg Leu Gln	788
209 214 219 224	
agt gac aat gag tac aag aag gac ttt gcc aag agt cg ^g tcc cag ttt Ser Asp Asn Glu Tyr Lys Asp Phe Ala Lys Ser Arg Ser Gln Phe	836
225 230 235 240	
cac agc agc aca gac cag ccc ggc ctc ctt cag gcc aag agg agc cag His Ser Ser Thr Asp Gln Pro Gly Leu Leu Gln Ala Lys Arg Ser Gln	884
241 246 251 256	
cag ctg gcc agt gat gtg cac tac agg cag ccc ctg ccc cag ccc acc Gln Leu Ala Ser Asp Val His Tyr Arg Gln Pro Leu Pro Gln Pro Thr	932
257 262 267 272	
tgc gac ccg gag cag ctg ggc ctc agg cat gct cag aag gcc cac cag Cys Asp Pro Glu Gln Leu Gly Leu Arg His Ala Gln Lys Ala His Gln	980
273 278 283 288	
ctg cag agt gat gtc aag tat aaa tca gac ttg aac ctg acc aga ggt Leu Gln Ser Asp Val Lys Tyr Lys Ser Asp Leu Asn Leu Thr Arg Gly	1028
289 294 299 304	
gtt ggc tgg acc cct cct ggc tcc tac aaa gtg gaa atg gct cg ^g cg ^g Val Gly Trp Thr Pro Pro Gly Ser Tyr Lys Val Glu Met Ala Arg Arg	1076
305 310 315 320	
gct gcg gaa ctg gcc aac gca agg ggc ctg ggt ctc cag gga gct tac Ala Ala Glu Leu Ala Asn Ala Arg Gly Leu Gly Leu Gln Gly Ala Tyr	1124
321 326 331 336	
cg ^g ggg gca gaa gca gtg gag gct gga gat cat cag agt ggg gag gtg Arg Gly Ala Glu Ala Val Glu Ala Gly Asp His Gln Ser Gly Glu Val	1172
337 342 347 352	
aac cca gat gcc act gag att ctg cac gtc aaa aag aag aag gcc ctg	1220

Asn Pro Asp Ala Thr Glu Ile Leu His Val Lys Lys Lys Lys Ala Leu
353 358 363 368

ctg ttg tga gccatgt ccaccctgat tcctgagagg ccagagagga agtttggta 1276
Leu Leu *
369

ccagagacag gcttcagatg gcttgattt cggcaagctg gaatggccca ccagccccatc 1336
ccagatcttc ctttattaaa ataataactc tgaaagcaaa aaaaaaa 1382

<210> 1101
<211> 1712
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (551)..(1672)

<400> 1101
caagctcgta aacgactcac tatagggaaa gctggtaacgc ctgcaggtac cggtccggaa 60

ttcccgggtc gacgatttcg tgccgggccc cggcgccgc gtcctcctca tcctccaggc 120

gacaagctgc ggctcagccc cactgacatt ggctcctgcc cgcctgcgg cccctgcccc 180

atcccgaagc cggcagccag aggcaggcgc cagagtcaag actggggcaa gagtgacgag 240

aggctgctac aagccgtgga aaacaacgt gcacccctggg tggccgcct catcgccgc 300

aaggggctgg tgcccacgaa gctagacccc gagggcaagt ccgcgttcca cctggcggcc 360

atgcggggtg cggccagctg tctggaggtg atgatagctc atggcagcaa tgtcatgagc 420

gcggacgggg caggttacaa tgccctccac ctggccgcca aatacggca cccacagtgc 480

ttgaagcaac tactgcaggc ttccctgcgtg gtggacgtcg tggacagcag cgggtggact 540

gccctacacc atg cag ggg tgg att gcc cta gca gcg gct ggt ggc tgt 589
Met Gln Gly Trp Ile Ala Leu Ala Ala Gly Gly Cys
1 5 10

ctc tcc tgc tca gag gtg ctc tgc tcc ttt aag gca cat cta aac ccc 637
Leu Ser Cys Ser Glu Val Leu Cys Ser Phe Lys Ala His Leu Asn Pro
14 19 24 29

caa gat cgg tca ggc gca aca ccc ctc att ata gca gct cag atg tgt 685
Gln Asp Arg Ser Gly Ala Thr Pro Leu Ile Ile Ala Ala Gln Met Cys
30 35 40 45

cac aca gac ctg tgc cgt ctc cta ctg cag caa ggg gct gcc gcg aac 733
His Thr Asp Leu Cys Arg Leu Leu Gln Gln Gly Ala Ala Ala Asn
46 51 56 61

gat cag gac ctg caa ggc agg acg gcc ctg atg ctg gcc tgt gag ggg Asp Gln Asp Leu Gln Gly Arg Thr Ala Leu Met Leu Ala Cys Glu Gly	781
62 67 72 77	
 gcc agc ccc gaa aca gtg gag gtc ctg ctg cag ggc gga gcc cag ccg Ala Ser Pro Glu Thr Val Glu Val Leu Leu Gln Gly Gly Ala Gln Pro	829
78 83 88 93	
 ggc atc acc gat gcg ctg ggg cag gac gcg gct cac tat ggc gcc ctg Gly Ile Thr Asp Ala Leu Gly Gln Asp Ala Ala His Tyr Gly Ala Leu	877
94 99 104 109	
 gcg ggg gac aaa ctc atc ctg cac ctt ctg caa gag gcg gcc cag cgc Ala Gly Asp Lys Leu Ile Leu His Leu Leu Gln Glu Ala Ala Gln Arg	925
110 115 120 125	
 ccc tcc cca ccc agc gcc ctc aca gag gat gat tca ggc gag gcg tca Pro Ser Pro Pro Ser Ala Leu Thr Glu Asp Asp Ser Gly Glu Ala Ser	973
126 131 136 141	
 tct cag aac tct atg tcc agc cat gga aag cag ggg gcc ccc aag aag Ser Gln Asn Ser Met Ser His Gly Lys Gln Gly Ala Pro Lys Lys	1021
142 147 152 157	
 cgg aag gcg cct cca cct ccc gcc agc att ccc atg ccg gat gat cga Arg Lys Ala Pro Pro Pro Ala Ser Ile Pro Met Pro Asp Asp Arg	1069
158 163 168 173	
 gat gcc tat gag gag atc gtg agg ctg cgg cag gag agg ggc cgc ctc Asp Ala Tyr Glu Glu Ile Val Arg Leu Arg Gln Glu Arg Gly Arg Leu	1117
174 179 184 189	
 ctg cag aag atc cgg ggc ctg gaa cag cac aag gaa cgg agg cag cag Leu Gln Lys Ile Arg Gly Leu Glu Gln His Lys Glu Arg Arg Gln Gln	1165
190 195 200 205	
 gag tcc ccg gag gcc agc tcc ctg cac atc ctg gag aga cag gtg caa Glu Ser Pro Glu Ala Ser Ser Leu His Ile Leu Glu Arg Gln Val Gln	1213
206 211 216 221	
 gag cta cag cag ttg ctg gtg gag aga caa gag gag aag gag agc ctg Glu Leu Gln Gln Leu Leu Val Glu Arg Gln Glu Glu Lys Glu Ser Leu	1261
222 227 232 237	
 gga cgg gag gtg gag agt ttg cag agc cgg ctg tcc ctg ctg gag aac Gly Arg Glu Val Glu Ser Leu Gln Ser Arg Leu Ser Leu Leu Glu Asn	1309
238 243 248 253	
 gag cgg gag aat act agc tat gac gta acc acc ctg cag gat gag gag Glu Arg Glu Asn Thr Ser Tyr Asp Val Thr Thr Leu Gln Asp Glu Glu	1357
254 259 264 269	
 ggt gag ctg cct gac ctt cca ggg gcc gag gtg ctg ctg tcc aga caa Gly Glu Leu Pro Asp Leu Pro Gly Ala Glu Val Leu Leu Ser Arg Gln	1405
270 275 280 285	

ctc agt ccg tcg gcc cag gaa cac ctg gcc tcg ctg cag gaa cag cgt		1453
Leu Ser Pro Ser Ala Gln Glu His Leu Ala Ser Leu Gln Glu Gln Val		
286 291 296 301		
gct gtg ctc acc aga cag aac cag gaa ctg atg gag aag gtc cag atc		1501
Ala Val Leu Thr Arg Gln Asn Gln Glu Leu Met Glu Lys Val Gln Ile		
302 307 312 317		
ctg gag aac ttt gag aag gac gag aca cag atg gaa gtg gaa gct ttg		1549
Leu Glu Asn Phe Glu Lys Asp Glu Thr Gln Met Glu Val Glu Ala Leu		
318 323 328 333		
gca gag gtc att cct ctt gcc ctt atg aat ctc tct cggtgcc gag ttt		1597
Ala Glu Val Ile Pro Leu Ala Leu Met Asn Leu Ser Arg Ala Glu Phe		
334 339 344 349		
gac cat ttc gca ggc aca cgc ttg agc ctt gag gcc ctg agg cag cag		1645
Asp His Phe Ala Gly Thr Arg Leu Ser Leu Glu Ala Leu Arg Gln Gln		
350 355 360 365		
gag aca cga gat gtc ccc aga gaa tag gggcc acctgtggga gagtgaggta		1697
Glu Thr Arg Asp Val Pro Arg Glu *		
366 371		
ctgagccacg ccact		1712

<210> 1102
 <211> 813
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (497)..(721)

<400> 1102		
ctgcacgtac cggccggaa ttccccggtc gacgatttcg taatatctcc agaaaataggg		60
ataacgctac tgatagttat tcattcgtat attagcggtt tttattgcaa ctggaaacg		120
ttaaaaatgg tgggtattcg atttttctct cgttttgtc aattcgattt tccacagtt		180
tggcacgccc cgtcaccaac ggcttaccgg atcggttcac agtaagccct acgatgaaat		240
gtgacaaaaaa ttgactttat tcagcaaaaa tgaaaatcag cccgctgaat atgtaacatt		300
aattaacccg aacaatacgg gcaaaaaaca ttcatgataa aaatatttat tggtcattat		360
atthaacgtat tttatagcac tgccgatatc acgctaaaaa aacaaccact gctattttta		420
gcaaagctta tggtatactc cgccgcctta acattttca ccgcaaattt tcattgcaac		480
atgacgagga aaataa atg agt acg cct gat ttt tct act gcc gag aat		529
Met Ser Thr Pro Asp Phe Ser Thr Ala Glu Asn		

1

5

aat caa gaa ctg gca aat gaa gtc tcc tgc ctg aaa gcg atg ctg acg				577
Asn Gln Glu Leu Ala Asn Glu Val Ser Cys Leu Lys Ala Met Leu Thr				
12	17	22	27	
ctg atg ctg cag gcg atg gga caa gct gac gcg ggc cgc gtg atg tta				625
Leu Met Leu Gln Ala Met Gly Gln Ala Asp Ala Gly Arg Val Met Leu				
28	33	38	43	
aag atg gaa aaa cag ctt gcg ctg atc gaa gac gaa acc cag gct gca				673
Lys Met Glu Lys Gln Leu Ala Leu Ile Glu Asp Glu Thr Gln Ala Ala				
44	49	54	59	
gta ttt tcc aaa acg gtt aag caa att aaa caa gcc tac cgt cag taa				721
Val Phe Ser Lys Thr Val Lys Gln Ile Lys Gln Ala Tyr Arg Gln *				
60	65	70	75	
tataaaaaccg gctgatagcg tgcctttcag ccggaaaaat catctggcac gcaggacaga				781
aaagagatca aatataagcca gtagccggccg ct				813

<210> 1103
<211> 1211
<212> DNA
<213> *Homo sapiens*

<220>
<221> CDS
<222> (541)..(1080)

<400> 1103

gtaaaaggcgg tagtgtgcc ccccaagaag ggtgtggc gcccgAACGG ttctgtcatt 60
cgTTTggatg gtaatgcgtg tgTTCTTgtg accaccacca gcgAGCAGCC tatcggtacg 120
cgtatTTTg ggCCGgtAAC tcgtgAGCTT cgtAGTgAGA agttcatgaa aattatctct 180
ctggcaccAG aagtactcta aggAGCgaAT catggcAGCG aaaatccgtc gtcATgacga 240
agttatcgtg ttaaccggta aagataaagg taaACGCGGT aaAGTtaAGA atgtcctgtc 300
ttccggcaag gtcattgttG aaggTatcaa CCTggTTAAG aaACATCAGA agccggTtCC 360
ggccctgaac caaccgggtg gcatcgTTGA AAAAGAAGCC gctattcagg tttccaACGT 420
agcaattttc aatgcggcaa ccggcaaggc tgaccgtgta ggcttagat tcgaAGACGG 480
taaaaaaAGTC cgTTTCTTCA agtctaACAG cgAAACTATC aagtaATTG gagTAGTACG 540
|
atg gCG aaa CTG cat gAT tac tac aaa gAC gAA gTA gTT aaa aaa CTC 588
Met Ala Lys Leu His Asp Tyr Tyr Lys Asp Glu Val Val Lys Lys Leu
1 5 10 15

atg act gag ttt aac tac aat tct gtc atg caa gtc cct cgg gtc gag			636
Met Thr Glu Phe Asn Tyr Asn Ser Val Met Gln Val Pro Arg Val Glu			
17	22	27	32
aag atc acc ctg aac atg ggt gtt ggt gaa gcg atc gct gac aaa aaa			684
Lys Ile Thr Leu Asn Met Gly Val Gly Ala Ile Ala Asp Lys Lys			
33	38	43	48
ctg ctg gat aac gca gca gca gac ctg gca gca atc tcc ggt caa aaa			732
Leu Leu Asp Asn Ala Ala Ala Asp Leu Ala Ala Ile Ser Gly Gln Lys			
49	54	59	64
ccg ctg atc acc aaa gca cgc aaa tct gtt gca ggc ttc aaa atc cgt			780
Pro Leu Ile Thr Lys Ala Arg Lys Ser Val Ala Gly Phe Lys Ile Arg			
65	70	75	80
cag ggc tat ccg atc ggc tgt aaa gta act ctg cgt ggc gaa cgc atg			828
Gln Gly Tyr Pro Ile Gly Cys Lys Val Thr Leu Arg Gly Glu Arg Met			
81	86	91	96
tgg gag ttc ttt gag cgc ctg atc act att gct gta cct cgt atc cgt			876
Trp Glu Phe Phe Glu Arg Leu Ile Thr Ile Ala Val Pro Arg Ile Arg			
97	102	107	112
gac ttc cgt ggc ctg tcc gct aag tct ttc gac ggt cgt ggt aac tac			924
Asp Phe Arg Gly Leu Ser Ala Lys Ser Phe Asp Gly Arg Gly Asn Tyr			
113	118	123	128
agc atg ggt gtc cgt gag cag atc atc ttc cca gaa atc gac tac gat			972
Ser Met Gly Val Arg Glu Gln Ile Ile Phe Pro Glu Ile Asp Tyr Asp			
129	134	139	144
aaa gtc gac cgc gtt cgt ggt ttg gat att acc att acc act act gcg			1020
Lys Val Asp Arg Val Arg Gly Leu Asp Ile Thr Ile Thr Thr Ala			
145	150	155	160
aaa tct gac gaa gaa ggc cgc gct ctg ctg gct gcc ttt gac ttc ccg			1068
Lys Ser Asp Glu Glu Arg Ala Leu Leu Ala Ala Phe Asp Phe Pro			
161	166	171	176
tcc cgc aag taa ggt agggttacta aatggctaag caatcaatga aagcacgcga			1123
Phe Arg Lys *			
177			
agtaaaaacgc gtagctttag ctgataaata cttcgcgaaa cgcgctgaac tgaaagcgat			1183
catctatgat gtgaacgctt ccgacgaa			1211

<210> 1104
 <211> 1327
 <212> DNA
 <213> Homo sapiens

<220>

<221> CDS
<222> (251)..(1300)

<400> 1104

accggccgg aattccggg tcgacgattt cggtgaactg caggtctctc cccagtggaa	60
agccccagag atgagccaga tctgcctcag ctgtggccat ccgtcagcgt aagggcccg	120
atgggcctct tggAACATTG gtgtgttcat ctgcattcga tgtgctggaa tccacaggaa	180
tctgggggtg cacatatcca gggtaaagtc agttaacctc gaccagtgga ctcaagaaca	240
gattcagtgc atg caa gag atg gga aat gga aag gca aac cga ctt tat	289
Met Gln Glu Met Gly Asn Gly Lys Ala Asn Arg Leu Tyr	
1 5 10	
gaa gcc tat ctt cct gag acc ttt cgg cga cct cag atg gac cca gct	337
Glu Ala Tyr Leu Pro Glu Thr Phe Arg Arg Pro Gln Met Asp Pro Ala	
14 19 24 29	
gtt gaa gga ttt att cga gac aaa tat gag aag aag aaa tac atg gac	385
Val Glu Gly Phe Ile Arg Asp Lys Tyr Glu Lys Lys Lys Tyr Met Asp	
30 35 40 45	
cga agt ctg gac atc aat gcc ttt agg aaa gaa aaa gat gac aag tgg	433
Arg Ser Leu Asp Ile Asn Ala Phe Arg Lys Glu Lys Asp Asp Lys Trp	
46 51 56 61	
aaa aga ggg agc gaa cca gtt cca gaa aaa aaa ttg gaa cct gtt gtt	481
Lys Arg Gly Ser Glu Pro Val Pro Glu Lys Lys Leu Glu Pro Val Val	
62 67 72 77	
ttt gag aag gtg aaa atg cca cag aaa aaa gaa gac cca cag cta cct	529
Phe Glu Lys Val Lys Met Pro Gln Lys Glu Asp Pro Gln Leu Pro	
78 83 88 93	
cgg aaa agc tcc ccg aaa tcc aca gcg cct gtc atg gat ttg ttg ggc	577
Arg Lys Ser Ser Pro Lys Ser Thr Ala Pro Val Met Asp Leu Leu Gly	
94 99 104 109	
ctt gat gct cct gtg gcc tgc tcc att gca aat agt aag acc agc aat	625
Leu Asp Ala Pro Val Ala Cys Ser Ile Ala Asn Ser Lys Thr Ser Asn	
110 115 120 125	
acc cta gag aag gat tta gat ctg ttg gcc tct gtt cca tcc cct tct	673
Thr Leu Glu Asp Leu Asp Leu Leu Ala Ser Val Pro Ser Pro Ser	
126 131 136 141	
tct tcg ggt tcc aga aag gtt gta ggt tcc atg cca act gca ggg agt	721
Ser Ser Gly Ser Arg Lys Val Val Gly Ser Met Pro Thr Ala Gly Ser	
142 147 152 157	
gcc ggc tct gtt cct gaa aat ctg aac ctg ttt ccg gag cca ggg agc	769
Ala Gly Ser Val Pro Glu Asn Leu Asn Leu Phe Pro Glu Pro Gly Ser	/
158 163 168 173	
aaa tca gaa gaa ata ggc aag aaa cag ctc tct aaa gac tcc att ctt	817

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Lys Ser Glu Glu Ile Gly Lys Lys Gln Leu Ser Lys Asp Ser Ile Leu				
174	179	184	189	
tca ctg tat gga tcc cag acg cct caa atg cct act caa gca atg ttc				865
Ser Leu Tyr Gly Ser Gln Thr Pro Gln Met Pro Thr Gln Ala Met Phe				
190	195	200	205	
atg gct ccc gct cag atg gca tat ccc aca gcc tac ccc agc ttc ccc				913
Met Ala Pro Ala Gln Met Ala Tyr Pro Thr Ala Tyr Pro Ser Phe Pro				
206	211	216	221	
ggg gtt aca cct cct aac agc ata atg ggg agc atg atg cct cca cca				961
Gly Val Thr Pro Pro Asn Ser Ile Met Gly Ser Met Met Pro Pro Pro				
222	227	232	237	
gta ggc atg gtt gct cag cca gga gct tct ggg atg gtt gcc ccc atg				1009
Val Gly Met Val Ala Gln Pro Gly Ala Ser Gly Met Val Ala Pro Met				
238	243	248	253	
gcc atg cct gca ggc tat atg ggt ggc atg cag gca tca atg atg ggt				1057
Ala Met Pro Ala Gly Tyr Met Gly Met Gln Ala Ser Met Met Gly				
254	259	264	269	
gtg ccg aat gga atg atg acc acc cag cag gct ggc tac atg gca ggc				1105
Val Pro Asn Gly Met Met Thr Thr Gln Gln Ala Gly Tyr Met Ala Gly				
270	275	280	285	
atg gca gct atg ccc cag act gtg tat ggg gtc cag cca gct cag cag				1153
Met Ala Ala Met Pro Gln Thr Val Tyr Gly Val Gln Pro Ala Gln Gln				
286	291	296	301	
ctg caa tgg aac ctt act cag atg acc cag cag atg gct ggg atg aac				1201
Leu Gln Trp Asn Leu Thr Gln Met Thr Gln Gln Met Ala Gly Met Asn				
302	307	312	317	
ttc tat gga gcc aat ggc atg atg aac tat gga cag tca atg agt ggc				1249
Phe Tyr Gly Ala Asn Gly Met Met Asn Tyr Gly Gln Ser Met Ser Gly				
318	323	328	333	
gga aat gga cag gca gca aat cag act ctc agt cct cag atg tgg aaa				1297
Gly Asn Gly Gln Ala Ala Asn Gln Thr Leu Ser Pro Gln Met Trp Lys				
334	339	344	349	
taa aaacaaaaaca cctgtaaaaaa aaaaaaaaa				1327
*				
350				